

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 27, 2004, 05:54:07 ; Search time 20 Seconds  
(without alignments)  
1519.826 Million cell updates/sec

Title: US-09-403-882A-2  
Perfect score: 1622  
Sequence: 1 MAEVLQESGGLVQPGSR.....VLTITSLIILMLWQKKPR 316

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_78.\*  
1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	892.5	55.0	268	2 A56446	Ig heavy chain V r
2	718.5	44.3	249	2 S41374	single chain Fv an
3	626.5	38.6	233	2 JC5322	p53 specific singl
4	555.5	34.2	213	2 S68213	Ig heavy chain (Ma
5	535	33.0	136	1 G1M821	Ig heavy chain pre
6	522.5	32.2	121	2 B34871	Ig heavy chain V r
7	516	31.8	130	1 JL0079	Ig kappa chain pre
8	514	31.7	235	2 S25058	Ig kappa chain - m
9	511	31.5	107	2 A30562	Ig kappa chain V r
10	508	31.3	103	2 S29591	Ig kappa chain V r
11	508	31.3	104	2 B49049	Ig kappa chain V r
12	506	31.2	106	2 F50071	Ig kappa chain V r
13	506	31.2	107	2 S30562	Ig kappa chain V r
14	501	30.9	107	2 S11118	Ig kappa chain V r
15	498	30.7	107	2 PC4405	Ig kappa chain V r
16	498	30.7	107	2 S11119	Ig kappa chain V r
17	490	30.2	107	2 S11121	Ig kappa chain V r
18	488	30.1	107	2 PT0406	Ig kappa chain V r
19	484.5	29.9	143	2 S23624	Ig heavy chain V r
20	483	29.8	107	2 S11117	Ig kappa chain V r
21	482	29.7	120	2 S12953	Ig heavy chain V r
22	481.5	29.7	108	2 G30560	Ig kappa chain V r
23	480	29.6	94	2 D25913	Ig heavy chain V r
24	479	29.5	100	2 S29590	Ig kappa chain V r
25	479	29.5	107	2 S11112	Ig kappa chain V r
26	478	29.3	108	2 PH1015	Ig heavy chain V r
27	476	29.3	107	2 PD0011	Ig kappa chain V r
28	473	29.2	97	2 PH1084	Ig light chain V r
29	473	29.2	114	2 S46392	Ig heavy chain V r

ALIGNMENTS

RESULT 1

A56446  
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)  
C:Species: Mus musculus (house mouse)  
C>Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996  
C:Accession: A56446  
R:Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.  
J. Biol. Chem. 270, 7829-7835, 1995  
A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical  
A:Reference number: A56446; MUID:95229583; PMID:7713873  
A:Accession: A56446  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-268 <TAN>  
A:Cross-references: GB:U20617  
C:Keywords: heterotetramer; immunoglobulin

Query Match	55.0%;	Score	892.5;	DB 2;	Length	268;
Best Local Similarity	65.9%;	Pred. No.	2.7e-52;			
Matches	176;	Conservative	26;	Mismatches	52;	Indels 13; Gaps 2;
QY	1	MAEVLQESGGLVQPGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAIYSSGSETI	60			
Db	1	MAQVKLQESGAEVLKPGASVKLSCTTSQFNKIDTYMHVVKORPEQGLEWIGRIAPANGIT	60			
QY	61	YYADTVKGRFTISRDNPKNLTFLQWTSLSRSDTYNYCA---RDYGAHWGGTIVTVSS	116			
Db	61	KYDPKFGKATIAADTSSNTAYLQLSLSSTEDTAVVYCASYLTTRYENWGGTIVTVSS	120			
QY	117	GGGGSGGGSGGGSDIELTQSPAIMASPGERTVMTCSASSVRYMNFQKSGTSPKR	176			
Db	121	GGGGSGGGSGGGSDIELTQSPAIMASLGEKVTMCRASSVNFIVYQKSDASPKL	180			
QY	177	WYDTSKLSSGVPAFPFGSGSGTYSVLTISMEAEADATYYCQWSSNPLTFGAGTKLEL	236			
Db	181	WYTYTSLPFGVPARFPGSGSGNSVLTISMEGEDATYYCQOFTSSPFTFGSGTKLEI	240			
QY	237	KKA-----AAEKLISEEDLNGA	254			
Db	241	KSAAHHHHHGAAEQKLISEEDLNGA	267			

RESULT 2

S41374  
single chain Fv antibody - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
C:Accession: S41374  
R:Artsenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.  
submitted to the EMBL Data Library, January 1994  
A:Description: Construction and functional characterization of a single chain Fv antibody  
A:Reference number: S41374

Ig heavy chain V r  
Ig heavy chain V r  
Ig heavy chain V r  
Ig heavy chain V r  
Ig heavy chain V r  
Ig heavy chain V r  
Ig kappa chain V r  
Ig epsilon chain C  
Ig light chain V r  
Ig kappa chain V r  
Ig heavy chain pre  
Ig light chain V r  
anti-D-dimer monoc  
Ig light chain V r  
Ig heavy chain V r  
Ig kappa chain pre  
Ig light chain V r



QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICAR----DYGA--YWGQGTVTYVS 116  
 DB 77 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARWGNYPYAMDYWGQGTVTYVS 136

RESULT 6  
 B34871  
 Ig heavy chain V region - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 15-Feb-1991 #sequence\_revision 13-Sep-1991 #text\_change 16-Aug-1996  
 C:Accession: B34871  
 R:Chaudhary, V.K.; Batra, J.K.; Gallo, M.G.; Willingham, M.C.; FitzGerald, D.J.; Pastan, Proc. Natl. Acad. Sci. U.S.A. 87, 1066-1070, 1990  
 A:Title: A rapid method of cloning functional variable-region antibody genes in Escherichia coli  
 A:Reference number: A34871; MUID:90138938; PMID:2105495  
 A:Accession: B34871  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-121 <CHA>  
 A:Cross-references: GB:M34000  
 A:Note: the authors translated the codon GTG for residue 119 as Gly  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMV>

Query Match 32.2%; Score 522.5; DB 2; Length 121;  
 Best Local Similarity 83.5%; Pred. No. 4.3e-28;  
 Matches 101; Conservative 7; Mismatches 6; Indels 7; Gaps 2;

QY 3 EVKLQBSGGGLVQPGGRKLSCAASGTFSSFGHWVRQAPKGLWVAYISSGSIYY 62  
 DB 1 DVQLVESGGGLVQPGGRKLSCAASGTFSSFGHWVRQAPKGLWVAYISRGNTIYY 60

QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARD--YG-----AYWGQGTVTYVS 115  
 DB 61 ADTVKGRFTISRDNPKNTLFLQMTSLRSDDTMYICARSYYGYFYAMDYWGQGTTLTVS 120

QY 116 S 116  
 DB 121 S 121

RESULT 7  
 JL0079  
 Ig kappa chain precursor V region (anti-phenylloxazalone 6F6) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 31-Dec-1991 #sequence\_revision 09-Aug-1996 #text\_change 16-Jul-1999  
 C:Accession: JL0079; A43044; E49044  
 R:Kaartinen, M.; Rocca-Serra, J.; Maekela, O. Mol. Immunol. 25, 859-865, 1988  
 A:Title: Combinatorial association of V genes: one VH gene codes for three non-cross-reactive V genes  
 A:Reference number: JL0076; MUID:89096973; PMID:3211160  
 A:Accession: JL0079  
 A:Molecule type: mRNA  
 A:Residues: 1-130 <KAA>  
 A:Cross-references: GB:M27792; NID:G197159  
 A:Experimental source: mRNA clones for anti-phenylloxazalone antibody 6F6  
 A:Note: the authors translated the codon TTC for residue 8 as Pro and TTC for residue 10 as Leu  
 R:Malstein, C.; Even, J.; Jarvis, J.M.; Gonzalez-Fernandez, A.; Gherardi, E. Eur. J. Immunol. 22, 1627-1634, 1992  
 A:Title: Non-random features of the repertoire expressed by the members of one V kappa gene  
 A:Reference number: A49044; MUID:92289826; PMID:1601044  
 A:Accession: A49044  
 A:Molecule type: DNA  
 A:Residues: 1-25 <MIL>  
 A:Cross-references: GB:G37663; NID:G250214; PIDN:AAB22331.1; PID:G250217  
 A:Note: sequence extracted from NCBI backbone (NCBIN:106802, NCBI:106809)  
 A:Accession: B49044  
 A:Molecule type: DNA  
 A:Residues: 114-116 <MIL2>  
 A:Cross-references: GB:G37664; NID:G250215; PIDN:AAB22332.1; PID:G250218  
 A:Experimental source: BALB/c germ-line

A:Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addi  
 A:Note: sequence extracted from NCBI backbone (NCBIN:106807, NCBI:106822)  
 C:Genetics:  
 A:Gene: V(kappa)Ox1  
 A:Introns: 17/1  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka  
 hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-130/Product: Ig kappa chain V region (6F6) #status predicted <MAT>  
 F:38-111/Domain: immunoglobulin homology <IMV>  
 F:45-109/Disulfide bonds: #status predicted

Query Match 31.8%; Score 516; DB 1; Length 130;  
 Best Local Similarity 92.5%; Pred. No. 1.3e-27;  
 Matches 99; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 133 IELTQSPAIMSASPGERVMTTCSSASSSVYVMWFOQKSGTSPKRWIYDTSKLSSGVPARF 192  
 DB 24 IVLTQSPAIMSASPGERVMTTCSSASSSVYVMWFOQKSGTSPKRWIYDTSKLSSGVPARF 83

QY 193 SGGSGTSTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLEKRA 239  
 DB 84 SGGSGTSTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLEKRA 130

RESULT 8  
 S25058  
 Ig kappa chain - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 21-Jan-2000  
 C:Accession: S25058  
 R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F. submitted to the EMBL Data Library, July 1992  
 A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific  
 A:Reference number: S25057  
 A:Accession: S25058  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-235 <FIS>  
 A:Cross-references: EMBL:X67211; NID:G54828; PIDN:CAA47650.1; PID:G54829  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 F:38-111/Domain: immunoglobulin homology <IMV>

Query Match 31.7%; Score 514; DB 2; Length 235;  
 Best Local Similarity 91.7%; Pred. No. 3.2e-27;  
 Matches 100; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 133 IELTQSPAIMSASPGERVMTTCSSASSSVYVMWFOQKSGTSPKRWIYDTSKLSSGVPARF 192  
 DB 24 IVLTQSPAIMSASPGERVMTTCSSASSSVYVMWFOQKSGTSPKRWIYDTSKLSSGVPARF 83

QY 193 SGGSGTSTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLEKRAA 241  
 DB 84 SGGSGTSTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLEKRAA 132

RESULT 9  
 A30562  
 Ig kappa chain V regions (27.7.2 and 27.4b.2) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 21-Jan-2000  
 C:Accession: A30562  
 R:Siikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.J. J. Immunol. 142, 888-893, 1989  
 A:Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-b  
 A:Reference number: A30562; MUID:89110066; PMID:2484031  
 A:Accession: A30562  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-107 <SIK>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 31.5%; Score 511; DB 2; Length 107;  
Best Local Similarity 91.5%; Pred. No. 2.2e-27;  
Matches 97; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
  
QY 133 IELTQSPAIMSASPGERVMTCTCSASSSVYNNWFQKSGTSPKRWIYDTSKLSSGVPARF 192  
DB 2 IVLTQSPAIMSASPGERVMTCTCSASSSVYNNWFQKSGTSPKRWIYDTSKLSSGVPARF 61  
  
QY 193 SSGSGTSSYSLTSSMEAEADATYCCQWSSNPLTFGAGTKLEK 238  
DB 62 SSGSGTSSYSLTSSMEAEADATYCCQWSSNPLTFGAGTKLEK 107

## RESULT 10

S29591  
Ig kappa chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C;Accession: S29591  
R;Kavaler, J.  
Submitted to the EMBL Data Library, April 1991  
A;Reference number: S26459  
A;Accession: S29591  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-103 <KAV>  
A;Cross-references: ENBL:X59094; NID:952227; PID:CAA1820.1; PID:952228  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-88/Domain: immunoglobulin homology <IMM>

Query Match 31.3%; Score 508; DB 2; Length 103;  
Best Local Similarity 94.2%; Pred. No. 3.3e-27;  
Matches 97; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
  
QY 133 IELTQSPAIMSASPGERVMTCTCSASSSVYNNWFQKSGTSPKRWIYDTSKLSSGVPARF 192  
DB 1 IVLTQSPAIMSASPGERVMTCTCSASSSVYNNWFQKSGTSPKRWIYDTSKLSSGVPARF 60

QY 193 SSGSGTSSYSLTSSMEAEADATYCCQWSSNPLTFGAGTKLE 235  
DB 61 SSGSGTSSYSLTSSMEAEADATYCCQWSSNPLTFGAGTKLE 103

## RESULT 11

B49049  
Ig kappa chain V region (anti-idiotypic) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C;Accession: B49049  
R;Armandola, E.A.; Mariani, S.M.; Zwickl, M.; Hardman, N.; Ferrone, S.  
Eur. J. Immunol. 22, 2893-2899, 1992  
A;Title: Molecular analysis of anti-idiotypic monoclonal antibodies in the HLA-DR antigen  
A;Reference number: A49049; MUID:93049629; PMID:1425914  
A;Accession: B49049  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-104 <ARM>  
A;Experimental source: BALB/c  
A;Note: sequence extracted from NCBI backbone (NCBI:118298, NCBI:118299)  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 31.3%; Score 508; DB 2; Length 104;  
Best Local Similarity 94.2%; Pred. No. 3.4e-27;  
Matches 97; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
  
QY 133 IELTQSPAIMSASPGERVMTCTCSASSSVYNNWFQKSGTSPKRWIYDTSKLSSGVPARF 192

DB 2 IVLTQSPAIMSASPGERVMTCTCSASSSVYNNWFQKSGTSPKRWIYDTSKLSSGVPARF 61  
  
QY 193 SSGSGTSSYSLTSSMEAEADATYCCQWSSNPLTFGAGTKLE 235  
DB 62 SSGSGTSSYSLTSSMEAEADATYCCQWSSNPLTFGAGTKLE 104

## RESULT 12

PS0071  
Ig kappa chain V region (38C13.V8) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 21-Jan-2000  
C;Accession: PS0071  
R;Levy, S.; Campbell, M.J.; Levy, R.  
J. Exp. Med. 170, 1-13, 1989  
A;Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangement  
A;Reference number: A92781; MUID:89310348; PMID:2501443  
A;Accession: PS0071  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-106 <LEV>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 31.2%; Score 506; DB 2; Length 106;  
Best Local Similarity 92.4%; Pred. No. 4.7e-27;  
Matches 97; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
  
QY 133 IELTQSPAIMSASPGERVMTCTCSASSSVYNNWFQKSGTSPKRWIYDTSKLSSGVPARF 192  
DB 2 IVLTQSPAIMSASPGERVMTCTCSASSSVYNNWFQKSGTSPKRWIYDTSKLSSGVPARF 61

QY 193 SSGSGTSSYSLTSSMEAEADATYCCQWSSNPLTFGAGTKLEK 237  
DB 62 SSGSGTSSYSLTSSMEAEADATYCCQWSSNPLTFGAGTKLEK 106

## RESULT 13

B30562  
Ig kappa chain V region (27.10.2) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 21-Jan-2000  
C;Accession: B30562  
R;Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.  
J. Immunol. 142, 888-893, 1989  
A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-b  
A;Reference number: A30562; MUID:89110066; PMID:2464031  
A;Accession: B30562  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-107 <SIK>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 31.2%; Score 506; DB 2; Length 107;  
Best Local Similarity 89.6%; Pred. No. 4.7e-27;  
Matches 95; Conservative 6; Mismatches 5; Indels 0; Gaps 0;  
  
QY 133 IELTQSPAIMSASPGERVMTCTCSASSSVYNNWFQKSGTSPKRWIYDTSKLSSGVPARF 192  
DB 2 IVLTQSPAIMSASPGERVMTCTCSASSSVYNNWFQKSGTSPKRWIYDTSKLSSGVPARF 61

QY 193 SSGSGTSSYSLTSSMEAEADATYCCQWSSNPLTFGAGTKLEK 238  
DB 62 SSGSGTSSYSLTSSMEAEADATYCCQWSSNPLTFGAGTKLEK 107

## RESULT 14

S1118  
Ig kappa chain V region (clone NQ5-61.1.2) - mouse (fragment)  
C;Species: Mus musculus (house mouse)

C>Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 21-Jan-2000  
C:Accession: S11118  
R:Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.  
Nature 304, 320-324, 1983  
A:Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone  
A:Reference number: S07331; MUID:83271467; PMID:6877353  
A:Accession: S11118  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-107 <KAA>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 30.9%; Score 501; DB 2; Length 107;  
Best Local Similarity 91.5%; Pred. No. 1e-26;  
Matches 97; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
QY 133 IELTQSPAIMSASGERVTMTCSASSSVRYMWFQKSGTSPKRWIYDTSKLSGGVPARF 192  
Db 2 IVLTSQPAIMSASPGKVTMTCSASSSVSYMHYQCKSGTSPKRWIYDTSKLSGGVPARF 61  
QY 193 SGSGSGTSYSLTISSMFAEDAATYYCQWSSNPLTFGAGTKLELKR 238  
Db 62 SGSGSGTSYSLTISSMFAEDAATYYCQWSSNPLTFGAGTKLELKR 107

RESULT 15  
PC4405  
Ig kappa chain V region (F3, anti-AFP) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 10-Nov-1997 #sequence\_revision 23-Jan-1998 #text\_change 21-Jan-2000  
C:Accession: PC4405  
R:Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.  
Chinese Biochem. J. 12, 648-653, 1996  
A:Title: Generation of a phage display library of the immunoglobulin repertoire from hum  
A:Reference number: PC4405  
A:Accession: PC4405  
A:Molecule type: mRNA  
A:Residues: 1-107 <DEN>  
A:Experimental source: spleen cell  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 30.7%; Score 498; DB 2; Length 107;  
Best Local Similarity 86.9%; Pred. No. 1.6e-26;  
Matches 93; Conservative 7; Mismatches 7; Indels 0; Gaps 0;  
QY 132 DIELTQSPAIMSASGERVTMTCSASSSVRYMWFQKSGTSPKRWIYDTSKLSGGVPAR 191  
Db 1 DIELTQSPAIMSASPGKVTMTCSASSSVSYMHYQCKSGTSPKRWIYDTSKLSGGVPAR 60  
QY 192 FSGSGSGTSYSLTISSMFAEDAATYYCQWSSNPLTFGAGTKLELKR 238  
Db 61 FSGSGSGTSYSLTISSMFAEDAATYYCQWSSNPLTFGAGTKLELKR 107

Search completed: May 27, 2004, 05:55:00  
Job time : 35 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 27, 2004, 05:54:07 ; Search time 18 Seconds  
(without alignments)  
914.120 Million cell updates/sec

Title: US-09-403-882A-2  
Perfect score: 1622  
Sequence: 1 MAEVKLQESGGLVQPGGSR.....VLTITSLILMLWQKPR 316

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	535	33.0	136	1 HV16_MOUSE	P01783 mus musculus
2	507	31.3	107	1 KV6F_MOUSE	P04940 mus musculus
3	506	31.2	107	1 KV6H_MOUSE	P04942 mus musculus
4	502	30.9	107	1 KV6I_MOUSE	P04943 mus musculus
5	500	30.8	107	1 KV6G_MOUSE	P04941 mus musculus
6	494	30.5	107	1 KV6J_MOUSE	P04944 mus musculus
7	446	27.5	107	1 KV6K_MOUSE	P01677 mus musculus
8	441	27.2	107	1 KV6L_MOUSE	P01676 mus musculus
9	440	27.1	107	1 KV6D_MOUSE	P01678 mus musculus
10	436	26.9	107	1 KV6A_MOUSE	P01675 mus musculus
11	433	26.7	108	1 KV6K_MOUSE	P04945 mus musculus
12	428	26.4	107	1 KV6E_MOUSE	P01679 mus musculus
13	425	26.2	114	1 HV3B_HUMAN	P01763 homo sapien
14	423	26.1	122	1 HV3G_HUMAN	P01768 homo sapien
15	418	25.8	117	1 HV54_MOUSE	P18525 mus musculus
16	416	25.6	119	1 HV37_MOUSE	P01807 mus musculus
17	414.5	25.6	121	1 HV3J_HUMAN	P01771 homo sapien
18	412	25.4	117	1 HV55_MOUSE	P18526 mus musculus
19	410	25.3	126	1 HV3K_HUMAN	P01772 homo sapien
20	407.5	25.1	115	1 HV32_MOUSE	P01801 mus musculus
21	407	25.1	119	1 HV40_MOUSE	P01810 mus musculus
22	404.5	24.9	113	1 HV30_MOUSE	P01799 mus musculus
23	403	24.8	119	1 HV38_MOUSE	P01808 mus musculus
24	402.5	24.8	111	1 HV41_MOUSE	P01811 mus musculus
25	402	24.8	116	1 HV3T_HUMAN	P01781 homo sapien
26	401.5	24.8	97	1 HV56_MOUSE	P18527 mus musculus
27	400.5	24.7	113	1 HV27_MOUSE	P01796 mus musculus
28	400	24.7	129	1 KV4A_MOUSE	P01680 mus musculus
29	399.5	24.6	115	1 HV33_MOUSE	P01802 mus musculus
30	397.5	24.5	113	1 HV29_MOUSE	P01798 mus musculus
31	396.5	24.4	113	1 HV31_MOUSE	P01800 mus musculus
32	394.5	24.3	113	1 HV28_MOUSE	P01797 mus musculus
33	394.5	24.3	118	1 HV39_MOUSE	P01809 mus musculus

## RESULT 1

HV16\_MOUSE  
 ID HV16\_MOUSE STANDARD; PRT; 136 AA.  
 AC 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 21-JUL-1986 (Rel. 01, Last annotation update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE IG heavy chain V region MOPC 21 precursor (Fragment).  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 CC NCBI\_TaxID=10090;  
 CC [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=81234548; PubMed=6788376;  
 RX Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.;  
 RA "Heavy chain variable region contribution to the NPB family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
 RL Cell 24:625-637(1981).  
 RN [2]  
 RP SEQUENCE OF 17-136.  
 RX MEDLINE=77100368; PubMed=401950;  
 RA Adetugbo K., Milstein C., Secher D.S.;  
 RL "Molecular analysis of spontaneous somatic mutants.";  
 RL Nature 265:299-304(1977).  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; J00522; AAD15290.1; -  
 DR PIR; E30809; GLMS21  
 DR PDB; 1IGC; 03-JUN-95.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 DR Immunoglobulin V region; Signal; 3D-structure.  
 KW NON\_TER 1  
 FT SIGNAL <1  
 FT CHAIN 17 136  
 FT DOMAIN 115 119  
 FT DOMAIN 120 136  
 FT DISULFID 38 112  
 FT CONFLICT 75 78  
 FT CONFLICT 89 90  
 FT CONFLICT 115 115  
 FT CONFLICT 120 120  
 FT CONFLICT 120 120  
 FT NON\_TER 136 136  
 SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;

P01805 rattus norv  
 P01767 homo sapien  
 P18528 mus musculus  
 P01785 canis famil  
 P01764 homo sapien  
 P01770 homo sapien  
 P01804 mus musculus  
 P01762 homo sapien  
 P01774 homo sapien  
 P01769 homo sapien  
 P01777 homo sapien  
 P01766 homo sapien

## ALIGNMENTS



```
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBT_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IGG response to 2-
  phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC
CC -!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
CC
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  or send an email to license@isb-sib.ch).
CC
CC EMBL; K00740; AAA38685.1; -.
DR HSSP; P01679; 2PBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11572 MW; 6F694824ECF0C8E6 CRC64;

Query Match 30.8%; Score 502; DB 1; Length 107;
Best Local Similarity 89.6%; Pred. No. 1.3e-30;
Matches 95; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 133 IELTQSPAINASPGERVVTTCSSASSSVRYNNFQKSGTSPKRWIYDTSKLSSGVPARF 192
Db 2 IVLQSPAINASPGQKVVTTCSSASSSVYNNFQKSGTSPKRWIYDTSKLSSGVPARF 61
QY 193 SGSGSGTSYSLTSSMEAEADAATYCCQWSSNPLTFGAGTKLELR 238
Db 62 SGSGSATSYSLTSSMQAEDAATYCCQWSSNPLTFGAGTKLELR 107

RESULT 5
KV6G MOUSE STANDARD; PRT; 107 AA.
AC P04941;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-VI region NQ2-48.2.2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBT_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IGG response to 2-
  phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC
CC -!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
CC
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CC
CC EMBL; K00740; AAA38685.1; -.
DR HSSP; P01679; 2PBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11572 MW; 6F694824ECF0C8E6 CRC64;

Query Match 30.8%; Score 502; DB 1; Length 107;
Best Local Similarity 89.6%; Pred. No. 1.3e-30;
Matches 95; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 133 IELTQSPAINASPGERVVTTCSSASSSVRYNNFQKSGTSPKRWIYDTSKLSSGVPARF 192
Db 2 IVLQSPAINASPGQKVVTTCSSASSSVYNNFQKSGTSPKRWIYDTSKLSSGVPARF 61
QY 193 SGSGSGTSYSLTSSMEAEADAATYCCQWSSNPLTFGAGTKLELR 238
Db 62 SGSGSATSYSLTSSMQAEDAATYCCQWSSNPLTFGAGTKLELR 107

RESULT 6
KV6J MOUSE STANDARD; PRT; 107 AA.
AC P04944;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-VI region NQ5-78.2.6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBT_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IGG response to 2-
  phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC
CC -!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
CC
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CC
CC EMBL; K00744; AAA38689.1; -.
DR HSSP; P01679; 2PBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
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CC
CC EMBL; K00737; AAA38682.1; -.
DR HSSP; P01679; 2PBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11556 MW; 72488DA9EF354934 CRC64;

Query Match 30.8%; Score 500; DB 1; Length 107;
Best Local Similarity 89.6%; Pred. No. 1.8e-30;
Matches 95; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 133 IELTQSPAINASPGERVVTTCSSASSSVRYNNFQKSGTSPKRWIYDTSKLSSGVPARF 192
Db 2 ILLTQSPAINASPGQKVVTTCSSASSSVYNNFQKSGTSPKRWIYDTSKLSSGVPARF 61
QY 193 SGSGSGTSYSLTSSMEAEADAATYCCQWSSNPLTFGAGTKLELR 238
Db 62 SGSGSATSYSLTSSMQAEDAATYCCQWSSNPLTFGAGTKLELR 107

RESULT 6
KV6J MOUSE STANDARD; PRT; 107 AA.
AC P04944;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-VI region NQ5-78.2.6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBT_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IGG response to 2-
  phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC
CC -!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
CC
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  or send an email to license@isb-sib.ch).
CC
CC EMBL; K00744; AAA38689.1; -.
DR HSSP; P01679; 2PBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
```



```
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11611 MW; A38290781F3C30D3 CRC64;

Query Match 30.5%; Score 494; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 4.9e-30;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 133 IELTQSPAIMSASPGERTVMTCSASSSVRYNWNFQKSGTSPKRWIYDTSKLSSGVPAF 192
Db 2 ILLTQSPAIMSASPGKVTMTCSASSSVRYNWNFQKSGTSPKRWIYDTSKLSSGVPAF 61
QY 193 SCGSGTGYSTLTSSMEAEADATYCCQWSSNPLTFGAGTKLELKR 238
Db 62 XGSGATSYLTSSMQAEADATYCCQWSSNPLTFGSGTKLEKR 107

RESULT 7
KV6C_MOUSE
ID KV6C_MOUSE STANDARD; PRT; 107 AA.
AC P01677;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region TEPC 601/TEPC 191.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (TEPC 601).
RX MEDLINE=79082830; PubMed=103573;
RA Rao D.N., Rudikoff S., Potter M.;
RT "k Chain variable regions from three galactan binding myeloma
proteins."
RL Biochemistry 17:5555-5559(1978).
RN [2]
RP SEQUENCE (TEPC 191).
RX MEDLINE=81054757; PubMed=6776525;
RA Rudikoff S., Rao D.N., Gaudemans C.P.J., Potter M.;
RT "kappa Chain joining segments and structural diversity of antibody
combining sites."
RL Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
CC -!- MISCELLANEOUS; THE TWO SEQUENCES ARE IDENTICAL.
CC -!- MISCELLANEOUS; THESE CHAINS WERE ISOLATED FROM MYELOMA PROTEINS
THAT BIND GALACTAN.
DR HSP; P01679; 2FBJ.
DR INTERPRO; IPR007110; IG-like.
DR INTERPRO; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11568 MW; 203CD752A5EC34D7 CRC64;
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```
Query Match 27.5%; Score 446; DB 1; Length 107;
Best Local Similarity 80.4%; Pred. No. 1.7e-26;
Matches 86; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 132 DIELTQSPAIMSASPGERTVMTCSASSSVRYNWNFQKSGTSPKRWIYDTSKLSSGVPAF 191
Db 1 EIVLTQSPAITAASLGQKVTITCSASSSVRYNWNFQKSGTSPKRWIYDTSKLSSGVPAF 60
QY 192 FSGSGTGYSTLTSSMEAEADATYCCQWSSNPLTFGAGTKLELKR 238
Db 61 FSGSGTGYSTLTSSMEAEADATYCCQWSSNPLTFGAGTKLELKR 107

RESULT 8
KV6B_MOUSE
ID KV6B_MOUSE STANDARD; PRT; 107 AA.
AC P01676;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region XRPC 24.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79082830; PubMed=103573;
RA Rao D.N., Rudikoff S., Potter M.;
RT "k Chain variable regions from three galactan binding myeloma
proteins."
RL Biochemistry 17:5555-5559(1978).
CC -!- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BIND GALACTAN.
DR HSP; P01679; 2FBJ.
DR INTERPRO; IPR007110; IG-like.
DR INTERPRO; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 33
FT DOMAIN 34 48
FT DOMAIN 49 55
FT DOMAIN 56 87
FT DOMAIN 88 96
FT DOMAIN 97 106
FT DISULFID 23 87
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11584 MW; 36B6D022A5EC34D7 CRC64;

Query Match 27.2%; Score 441; DB 1; Length 107;
Best Local Similarity 78.5%; Pred. No. 4.1e-26;
Matches 84; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 132 DIELTQSPAIMSASPGERTVMTCSASSSVRYNWNFQKSGTSPKRWIYDTSKLSSGVPAF 191
Db 1 EIVLTQSPAITAASLGQKVTITCSASSSVRYNWNFQKSGTSPKRWIYDTSKLSSGVPAF 60
QY 192 FSGSGTGYSTLTSSMEAEADATYCCQWSSNPLTFGAGTKLELKR 238
Db 61 FSGSGTGYSTLTSSMEAEADATYCCQWSSNPLTFGAGTKLELKR 107

RESULT 9
KV6D_MOUSE
ID KV6D_MOUSE STANDARD; PRT; 107 AA.
AC P01678;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
```

Query Match 26.7%; Score 433; DB 1; Length 108;



[illegible][illegible]

```

J. Exp. Med. 169:2007-2019(1989).
-1- MTSCELLANEUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
PIR, JTO505; HVMS84.
HSP; P01810; 2PBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SMC0406; IgV; 1.
PROSITE; PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 49 FRAMEWORK-1.1 REGION 5-84.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query March 25.8%; Score 418; DB 1; Length 117;
Best Local Similarity 79.0%; Pred. No. 2.3e-24;
Matches 79; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MAEVKLOESGGIVQPGGSRKLSCAASGFTFSFGMHVYQAPKGLWVAYISGGSTI 60
Db 18 LCEVKLVESGGIVQPGGSLKLSCAASGFTFSYTMWVRQTPKRLWVAYISNGGST 77
Qy 61 YYADTVKGRFTISRDNPQNTFLQMTSLRSEDTWYYCAR 100
Db 78 YYPDTVKGRFTISRDNAKNLYLQMSLSKSEDTAMYCAR 117

Search completed: May 27, 2004, 05:57:06
Job time : 20 secs

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 27, 2004, 05:54:07 ; Search time 50 Seconds  
(without alignments)  
1994.075 Million cell updates/sec

Title: US-09-403-882A-2  
Perfect score: 1622  
Sequence: 1 MAEVLQESGGGLVQPGGSR.....VLTITSLILMLWOKKPR 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archesp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	853.5	52.6	298	11 Q9YF0	Q9YF0 mus musculus
2	695	42.8	241	11 Q921A6	Q921A6 mus musculus
3	658	40.6	243	11 Q7TQM2	Q7TQM2 mus musculus
4	608.5	37.5	218	11 Q925S1	Q925S1 mus musculus
5	542	33.4	473	11 Q91205	Q91205 mus musculus
6	498	30.7	112	11 Q8K1F0	Q8K1F0 mus musculus
7	491	30.3	235	11 Q91W12	Q91W12 mus musculus
8	484.5	29.9	487	11 Q99KA4	Q99KA4 mus musculus
9	483	29.8	134	11 Q8VDD0	Q8VDD0 mus musculus
10	480	29.6	112	11 Q8K1F2	Q8K1F2 mus musculus
11	462.5	28.5	113	4 Q9UL90	Q9UL90 homo sapien
12	462	28.5	613	4 Q8WUK1	Q8WUK1 homo sapien
13	461	28.4	112	11 Q8K1F3	Q8K1F3 mus musculus
14	458	28.2	114	11 Q8K1F1	Q8K1F1 mus musculus
15	454.5	28.0	437	11 Q9P1A4	Q9P1A4 mus musculus
16	454.5	28.0	597	4 Q96BB9	Q96BB9 homo sapien

17	452.5	27.9	119	11 Q920E7	Q920E7 mus musculus
18	445	27.4	118	4 Q9UL91	Q9UL91 homo sapien
19	443	27.3	479	11 Q91WP5	Q91WP5 mus musculus
20	440.5	27.2	116	4 Q9UL93	Q9UL93 homo sapien
21	439.5	27.1	494	4 Q96K68	Q96K68 homo sapien
22	439	27.1	486	11 Q91207	Q91207 mus musculus
23	438.5	27.0	131	11 Q811C3	Q811C3 mus musculus
24	437	26.9	106	5 Q9U410	Q9U410 schistosoma
25	433.5	26.7	147	4 Q9Y509	Q9Y509 homo sapien
26	429	26.4	487	11 Q80Z17	Q80Z17 mus musculus
27	428	26.4	235	11 Q7TMK0	Q7TMK0 mus musculus
28	428	26.4	573	4 Q8WU38	Q8WU38 homo sapien
29	424	26.1	480	11 Q91XE1	Q91XE1 mus musculus
30	422	26.0	122	4 Q9UL84	Q9UL84 homo sapien
31	421.5	26.0	121	4 Q9UL71	Q9UL71 homo sapien
32	416	25.6	499	4 Q8N5K4	Q8N5K4 homo sapien
33	415	25.6	118	4 Q9UL72	Q9UL72 homo sapien
34	410	25.3	493	4 Q8NCL6	Q8NCL6 homo sapien
35	405	25.0	470	4 Q7Z5W1	Q7Z5W1 homo sapien
36	401.5	24.8	97	11 Q9JL76	Q9JL76 mus musculus
37	398.5	24.6	469	11 Q8R3V9	Q8R3V9 mus musculus
38	395	24.4	112	4 Q9HCC1	Q9HCC1 homo sapien
39	393.5	24.3	479	11 Q7TMK4	Q7TMK4 mus musculus
40	390.5	24.1	484	11 Q8VZA0	Q8VZA0 mus musculus
41	385	23.7	482	4 Q7Z351	Q7Z351 homo sapien
42	378.5	23.3	170	11 Q925S2	Q925S2 mus musculus
43	376	23.2	95	4 Q9ULB6	Q9ULB6 homo sapien
44	375.5	23.2	521	4 Q8N4Y9	Q8N4Y9 homo sapien
45	367.5	22.7	131	4 Q9UL88	Q9UL88 homo sapien

#### ALIGNMENTS

RESULT 1

Q9YF0 PRELIMINARY; PRT; 298 AA.

ID Q9YF0; 01-MAY-2000 (TRENBLrel. 13, Created)

AC Q9YF0; 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

DE CN 8 scfv.

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Balb/c; TISSUE=Spleen;

RX MEDLINE=20183931; PubMed=10706631;

RA Shinohara N., Demura T., Fukuda H.,

RT "Isolation of a vascular cell wall-specific monoclonal antibody

RT recognizing a cell polarity by using a phage display subtraction

RT method."

RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).

DR EMBL; AB036341; BAA86633.1; --

DR PIR; A33933; A33933.

DR PIR; S19112; S19112.

DR HSRF; P01607; IREI.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 2.

DR SMART; SM00406; IGV; 2.

DR PROSITE; PS00835; IG LIKE; 2.

SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 52.6%; Score 853.5; DB 11; Length 298;

Best Local Similarity 66.3%; Pred. No. 8.9e-60;

Matches 163; Conservative 32; Mismatches 46; Indels 5; Gaps 2;

QY 1 MAEVLQESGGGLVQPGGSRKLSAASGFTFSFGMHWVQAPKGLWVAYVSSGSSI 60

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Db 38 MAQVKLQSGGGLVPGGSLKLSAASGSDFSRYVMWVRQAPGKGLWGEINPDSTI 97
QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICAR-----DYGAYWQGGTTVTYSS 116
Db 98 NYTSLDKKFIISRDNKNTLYLQMSKVRSEDYLYCARASYYGHGAYWQGGTTVTYSS 157
QY 117 GGGSGGGGGGGGGGDIELTQSPALMSASPERVTMTCSASSV-RYMNWFOQKSGTSPK 175
Db 158 GGGSGGGGGGGGGGDIELTQSPALMSASVGTVTITCRAGNHNHVLAWYQKQKSPQ 217
QY 176 RWIYDTSKLSSGVPARFSGSGGTYSLSITSSMEABDAATYCCQWSSNPLTFGAGTKLE 235
Db 218 LLVYNNAKTLADGVPFRFSGSGGTQYSLKINSLOPEDFGSYCQHFHTTPTFFGGTKLE 277
QY 236 LKRAAA 241
Db 278 IKRAAA 283

RESULT 2
Q921A6 PRELIMINARY; PRT; 241 AA.
AC Q921A6;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Anti-CEA 79 single chain Fv fragment (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scfv).";
RL Mol. Cells 7:816-819(1997).
DR EMBL; U88067; AAB48044.1; -.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; Igv; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

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Query Match 42.8%; Score 695; DB 11; Length 241;
Best Local Similarity 55.7%; Pred. No. 2.7e-47;
Matches 137; Conservative 40; Mismatches 55; Indels 14; Gaps 5;

QY 3 EVKLQESGGGLVPGGSRKLSAASGFTFSSFGMHVWRQAPKGLWVAYISSGSIYY 62
Db 1 QVKLQOSGPFLKKGTEYKISCKASGYFTDYGNWYKQAPKGLKMGWINTVGEPTY 60
QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICAR-----YGVWQGGTTVTYSSGG 118
Db 61 ADDFKGRFAFLSASTAYLQINLNKNEATATYFCARKDILLYFDYWGQTTVTYSSGG 120
QY 119 GSGSGGGGGGGGDIELTQSPALMSASPERVTMTCSASSV-RYMNWFOQKSGTSPK- 176
Db 121 GSGSGGGGGGGGDIELTQSPALMSASVGTVTITCRAGNHNHVLAWYQKQKSPQ 180
QY 177 ---WYIYDTSKLSSGVPARFSGSGGTYSLSITSSMEABDAATYCCQWSSNPLTFGAGTK 233
Db 181 HTLHY----IQGIPSRFSGSGGSDYSPSISNLEPDIATYICLHY-DNLHTFGGQTK 235
QY 234 LELKEA 239
Db 236 LELKEA 241

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RESULT 3
Q7TQM2 PRELIMINARY; PRT; 243 AA.
AC Q7TQM2;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE scfv 6H8 protein (Fragment).
GN SCFV 6H8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Peter J.C., Eitekhari P., Billiald P., Wallukat G.;
RA "scfv single chain antibody variable fragment as inverse agonist for
RT the beta-2 adrenergic receptor.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ574851; CAE00495.1; -.
FT NON_TER 1
FT NON_TER 243
SQ SEQUENCE 243 AA; 25976 MW; BEFF64D2DCF4F76 CRC64;

Query Match 40.6%; Score 658; DB 11; Length 243;
Best Local Similarity 53.1%; Pred. No. 2.4e-44;
Matches 127; Conservative 43; Mismatches 63; Indels 6; Gaps 4;

QY 3 EVKLQESGGGLVPGGSRKLSAASGFTFSSFGMHVWRQAPKGLWVAYISSGSIYY 62
Db 1 QVKLQOSGPFLKKGTEYKISCKASGYFTDYGNWYKQAPKGLKMGWINTVGEPTY 60
QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGA--YWGQTTVTYSSGGGG 120
Db 61 DEKFNKGLITVDTSSSTAYMHLSSLAESDAVYICARGRGLDWGAGTTLTVSSGGGG 120
QY 121 GSGSGGGGGGDIELTQSPALMSASPERVTMTCSASSV-RYMNWFOQKSGTSPKRIY 179
Db 121 GSGSGGGGGGDIQMTQSSSFVSGLGRVITTCASEDIYNRLAWYQKQKGNAPRLTIS 180
QY 180 DTSKLSGGVPARFSGSGGTYSLSITSSMEABDAATYCCQ--WSSNPLTFGAGTKLELK 237
Db 181 GATSLTGVPSRFSGSGGKDYLSITSLQTEDVATYICQWSTR--TFGGTKLEIK 237

RESULT 4
Q925S1 PRELIMINARY; PRT; 218 AA.
AC Q925S1;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE MRP5 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RX PubMed=11819679;
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RC STRAIN=BALB/c;
RT "Cloning of mouse genes related to repairing of intestinal epithelium

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RT of the irradiated mice by treatment with the intestinal RNA of mice of the same strain."

RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80 (2001).

DR EMBL; AF240168; AA43733.1; .

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 2.

DR SMART; SMO0406; IGV; 1.

DR PROSITE; PS50835; IG LIKE; 1.

FT NON TER 218

SQ SEQUENCE 218 AA; 527E4FABF7982817 CRC64;

Query Match 37.5%; Score 608.5; DB 11; Length 218;

Best Local Similarity 55.5%; Pred. No. 1.8e-40;

Matches 121; Conservative 33; Mismatches 55; Indels 9; Gaps 3;

QY 1 MAEVKIQESGGGLVOPGSGSKLCAASGFTFSFGHWHVRQAPKGLGWVAVISSGSI 60

DB 1 MAQVKLOQSGPELKKGTEVIRISCKASGYFTTAGQWQVQKPKGLKRWGINTHSGVP 60

QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICAR-DYG---AYWGQGTIVTSS 116

DB 61 KYAEFPKGRPAFLSASTAYLIQISNLKQEDTATYFCMRWDYDGGFAVWGQGTIVTSS 120

QY 117 GGGSGGGGGGGGGGDIETQSPAIMSASGERVTWTCASSSV-----RYMWNFQOKSG 171

DB 121 GGGSGGGGGGGGGSDIVLTQSPASLAVSLGQRTISCRASVDNIGISFMWNFQOKSG 180

QY 172 TSPKRWIYDTSKLSGGVPARFSGSGTYSYLTSSME 209

DB 181 QPKLLIYAASKQSGVPAGLLASGSGTDFSLNIYPME 218

RESULT 5

Q91Z05 PRELIMINARY; PRT; 473 AA.

AC Q91Z05; (T-EMBLrel. 19, Created)

DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN AU044919.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC010327; AAH10327.1; .

DR MGD; MGI; 2144967; AU044919.

DR GO; GO:0005489; P:electron transporter activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR000345; Cyt c heme\_B.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 3.

DR SMART; SMO0406; IGV; 1.

DR PROSITE; PS00190; CYTOCHROME C; 1.

DR PROSITE; PS50835; IG LIKE; 4.

DR PROSITE; PS00290; IG\_MHC; 1.

KW Hypothetical protein\_1.

SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 33.4%; Score 542; DB 11; Length 473;

Best Local Similarity 51.7%; Pred. No. 9.3e-35;

Matches 120; Conservative 20; Mismatches 52; Indels 40; Gaps 5;

QY 3 EVKIQESGGGLVOPGSGSKLCAASGFTFSFGHWHVRQAPKGLGWVAVISSGSI 62

DB 20 EVLVESGGGLVOPGSGSKLCAASGFTFSFGHWHVRQAPKGLGWVAVISSGSI 79

RT of the irradiated mice by treatment with the intestinal RNA of mice of the same strain."

RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80 (2001).

DR EMBL; AF240168; AA43733.1; .

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 2.

DR SMART; SMO0406; IGV; 1.

DR PROSITE; PS50835; IG LIKE; 1.

FT NON TER 218

SQ SEQUENCE 218 AA; 527E4FABF7982817 CRC64;

Query Match 37.5%; Score 608.5; DB 11; Length 218;

Best Local Similarity 55.5%; Pred. No. 1.8e-40;

Matches 121; Conservative 33; Mismatches 55; Indels 9; Gaps 3;

QY 1 MAEVKIQESGGGLVOPGSGSKLCAASGFTFSFGHWHVRQAPKGLGWVAVISSGSI 60

DB 1 MAQVKLOQSGPELKKGTEVIRISCKASGYFTTAGQWQVQKPKGLKRWGINTHSGVP 60

QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICAR-DYG---AYWGQGTIVTSS 116

DB 61 KYAEFPKGRPAFLSASTAYLIQISNLKQEDTATYFCMRWDYDGGFAVWGQGTIVTSS 120

QY 117 GGGSGGGGGGGGGGDIETQSPAIMSASGERVTWTCASSSV-----RYMWNFQOKSG 171

DB 121 GGGSGGGGGGGGGSDIVLTQSPASLAVSLGQRTISCRASVDNIGISFMWNFQOKSG 180

QY 172 TSPKRWIYDTSKLSGGVPARFSGSGTYSYLTSSME 209

DB 181 QPKLLIYAASKQSGVPAGLLASGSGTDFSLNIYPME 218

RESULT 5

Q91Z05 PRELIMINARY; PRT; 473 AA.

AC Q91Z05; (T-EMBLrel. 19, Created)

DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN AU044919.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC010327; AAH10327.1; .

DR MGD; MGI; 2144967; AU044919.

DR GO; GO:0005489; P:electron transporter activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR000345; Cyt c heme\_B.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 3.

DR SMART; SMO0406; IGV; 1.

DR PROSITE; PS00190; CYTOCHROME C; 1.

DR PROSITE; PS50835; IG LIKE; 4.

DR PROSITE; PS00290; IG\_MHC; 1.

KW Hypothetical protein\_1.

SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 33.4%; Score 542; DB 11; Length 473;

Best Local Similarity 51.7%; Pred. No. 9.3e-35;

Matches 120; Conservative 20; Mismatches 52; Indels 40; Gaps 5;

QY 3 EVKIQESGGGLVOPGSGSKLCAASGFTFSFGHWHVRQAPKGLGWVAVISSGSI 62

DB 20 EVLVESGGGLVOPGSGSKLCAASGFTFSFGHWHVRQAPKGLGWVAVISSGSI 79

QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYCA-----YWGQGTIVTSSGG 118

DB 80 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARELWLRIDYWGQGTIVTSSA- 138

QY 119 GSGSGGGGGGGGDIETQSPAIMSASGERVTWTCASSSVRYMWNFQOKSGTSPKRW 178

DB 139 -----KTPPSVYPLAPGCGDTGTGSSVTGLCGLVKGYFPESVTVT----- 177

QY 179 YDTSKLSGGV---PARFSGSGSGTYSYLTSSMEAEADAATYYCQWSSNPLT 227

DB 178 WNSGLSSSVHTFPALLQSLGYTWSSSVTPES-----STWPSQTVT 218

RESULT 6

Q8K1F0 PRELIMINARY; PRT; 112 AA.

AC Q8K1F0; (T-EMBLrel. 22, Created)

DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE Anti-Vipase light chain variable region (Fragment).

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;

RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;

RT "Immune proteolytic antibodies: Failed D-vipase response to the D-

RT entanionomer of VIP and identification of L-vipase VL domains."

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF516285; AAM64203.1; .

DR PIR; A33933; A33933.

DR InterPro; IPR003599; Ig-like.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SMO0409; IGV; 1.

DR SMART; SMO0406; IGV; 1.

DR PROSITE; PS50835; IG LIKE; 1.

FT NON TER 1

FT NON TER 112

SQ SEQUENCE 112 AA; 11901 MW; F6644663201AA239 CRC64;

Query Match 30.7%; Score 498; DB 11; Length 112;

Best Local Similarity 88.8%; Pred. No. 4.5e-32;

Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 135 LTQSPAIMSASGERVTWTCASSSVRYMWNFQOKSGTSPKRWIYDTSKLSGGVPARFSG 194

DB 4 LTQSPAIMSASGERVTWTCASSSVRYMWNFQOKSGTSPKRWIYDTSKLSGGVPARFSG 63

QY 195 SSGTYSYLTSSMEAEADAATYYCQWSSNPLTFGAGTKLELRAAA 241

DB 64 SSGNSYSLTISSTEGEDATYYCQWSSNPLTFGGTKLEIKRADA 110

RESULT 7

Q91W12 PRELIMINARY; PRT; 235 AA.

AC Q91W12; (T-EMBLrel. 19, Created)

DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE Hypothetical protein.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

```
RC TISSUE-Breast tumor;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AAH06643.1; -.
DR PDB; 1AV1; 30-JAN-02.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS08135; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ
  Query Match      30.3%; Score 491; DB 11; Length 235;
  Best Local Similarity 87.2%; Pred. No. 4.2e-31;
  Matches 95; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 133 IELTOSPAIMASPGERTVMTCSASSSVRYNWNWFOQKSGTSPKRWIYDTKLSGVPARF 192
Db 24 IVLTQSPAIMASPGERTVMTCSASSSVRYNWNWFOQKSGTSPKRWIYDTKLSGVPDRF 83

QY 193 SGSGSGTGYSLTISMEAEADAATYCCQWSSNPLTFGAGTKLELKRAAA 241
Db 84 SGSGSGTGYSLTISNWEAEADAATYCCQWSSNPLTFGAGTKLELKRAA 132

RESULT 8
Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DE 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004786; AAH04786.1; -.
DR HSP; P01810; 2PBT.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS08135; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ
  Query Match      29.9%; Score 484.5; DB 11; Length 487;
  Best Local Similarity 41.6%; Pred. No. 3.6e-30;
  Matches 124; Conservative 23; Mismatches 72; Indels 79; Gaps 11;

QY 3 EVKLQESGGGLVQGGGRKLSAASGTFPSFGNHWVRQAPBKLEWAVISSGSTIYY 62
Db 20 EVQLVESGGGLVQGGGRKLSAASGTFPSFGNHWVRQAPBKLEWAVISSGSTIYY 79

QY 63 ADTVKGRFTISDRNPKNLFLQMTSLRSEDVTMYCYARDYGA-----YWGQGTIV 112
Db 80 PDNVKGRFTISDRNKNLYLQMSHLKASEDTAMNYCARDMGSPYGGYRFDYWGQGTII 139

QY 113 TVSSGGGGGGGGGGGGSDIELTQSPAI-----MSASPGERTVMTCSASSSVRYN 164
Db 140 TVSS-----ESARNPTIYPLTLPALSSDP---VLIIGLIH-----D 173

QY 165 WFQOKSGTSPKRWIYDTKLSGVP-----PARPSGSGSGTGYSLTISMEAEADAATYIC 218

Query Match      29.8%; Score 483; DB 11; Length 134;
Best Local Similarity 86.2%; Pred. No. 8.8e-31;
Matches 94; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 133 IELTOSPAIMASPGERTVMTCSASSSVRYNWNWFOQKSGTSPKRWIYDTKLSGVPARF 192
Db 24 IVLTQSPAIMASPGERTVMTCSASSSVRYNWNWFOQKSGTSPKRWIYDTKLSGVPARF 83

QY 193 SGSGSGTGYSLTISMEAEADAATYCCQWSSNPLTFGAGTKLELKRAAA 241
Db 84 SGSGSGTGYSLTISNWEAEADAATYCHORSSYPWTFGGTGLEIKRADA 132

RESULT 10
Q8K1F2 PRELIMINARY; PRT; 112 AA.
AC Q8K1F2;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DE 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Anti-Vipase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RA "Innate proteolytic antibodies: Failed D-Vipase response to the D-
RT entantioner of Vip and identification of L-Vipase VL domains.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

Query Match      29.8%; Score 483; DB 11; Length 134;
Best Local Similarity 86.2%; Pred. No. 8.8e-31;
Matches 94; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 133 IELTOSPAIMASPGERTVMTCSASSSVRYNWNWFOQKSGTSPKRWIYDTKLSGVPARF 192
Db 24 IVLTQSPAIMASPGERTVMTCSASSSVRYNWNWFOQKSGTSPKRWIYDTKLSGVPARF 83

QY 193 SGSGSGTGYSLTISMEAEADAATYCCQWSSNPLTFGAGTKLELKRAAA 241
Db 84 SGSGSGTGYSLTISNWEAEADAATYCHORSSYPWTFGGTGLEIKRADA 132
```



DR EMBL; AF516283; AAM64201.1; --  
 DR PIR; H33932; H33932.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SMO0406; IG; 1.  
 DR PROSITE; PS00406; IG; 1.  
 DR PROSITE; PS0835; IG-LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 112  
 FT NON\_TER 113  
 SQ SEQUENCE 112 AA; 11953 MW; 4716887FADBS43ED CRC64;  
 Query Match 29.6%; Score 480; DB 11; Length 112;  
 Best Local Similarity 86.4%; Pred. No. 1.2e-30;  
 Matches 95; Conservative 5; Mismatches 10; Indels 0; Gaps 0;  
 QY 132 DIETQSPAINASPGERVMTCSASSSVRYMNFQOKSGTSPKRWITDTSKLSGVPAR 191  
 Db 1 DIVLTQSPAINASPGSKVITTCNASSSVSYMHWFQOKPGTSPKLTWYSTNLSASGVPAR 60  
 QY 192 FSGSGSGTYSLTSSMEADAAATYCCQWSSNLTFTGAGTKLEKRAA 241  
 Db 61 FSGSGSGTISLTISRMEADAAATYCCQWSSNLTFTGAGTKLEKRAA 110

RESULT 11  
 Q9UL90 PRELIMINARY; PRT; 113 AA.  
 AC Q9UL90  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
 DR EMBL; AF035024; AAD56260.1; --  
 DR HSSP; P01772; 2FBA.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SMO0406; IG; 1.  
 DR PROSITE; PS00406; IG; 1.  
 DR PROSITE; PS0835; IG-LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 113  
 FT NON\_TER 114  
 SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;  
 Query Match 28.5%; Score 462.5; DB 4; Length 113;  
 Best Local Similarity 77.2%; Pred. No. 3e-29;  
 Matches 88; Conservative 10; Mismatches 15; Indels 1; Gaps 1;

QY 3 EVKLQESGGVLPQGGSRKLSCAASGFTFSFGHWHVQAPKGLWAVIISGSGSTIY 62  
 Db 1 EVQLVESGGGVLPQGGSRKLSCAASGFTFSFGHWHVQAPKGLWAVIIRYDGSNKY 60  
 QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVVMYICARDYAGYWGQTTVTYSS 116  
 Db 61 ADSVKGRFTISRDNPKNTLYLQMNLSRAEDTAVYICAKDLN-IWGQTLVTYSS 113

RESULT 12  
 Q8WUK1

ID Q8WUK1 PRELIMINARY; PRT; 613 AA.  
 AC Q8WUK1  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tissue-Tensil;  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC020240; AAH20240.1; --  
 DR PIR; P0120; P0120.  
 DR PIR; S15590; S15590.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG; 5.  
 DR SMART; SMO0406; IG; 1.  
 DR PROSITE; PS0835; IG-LIKE; 5.  
 DR PROSITE; PS0290; IG\_MHC; 3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;  
 Query Match 28.5%; Score 462; DB 4; Length 613;  
 Best Local Similarity 31.3%; Pred. No. 3e-28;  
 Matches 128; Conservative 46; Mismatches 111; Indels 124; Gaps 11;  
 QY 3 EVKLQESGGVLPQGGSRKLSCAASGFTFSFGHWHVQAPKGLWAVIISGSGSTIY 62  
 Db 20 QVQLVESGGGVLPQGGSRKLSCAASGFTFSFGHWHVQAPKGLWAVIISGSGNKY 79  
 QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVVMYICARDYAGYWGQTTVTYSS 116  
 Db 80 ADSVKGRFTISRDNPKNTLYLQMNLSRAEDTAVYICAKDLN-IWGQTLVTYSS 139  
 QY 117 GGGG-----SGGGSGGG-----GSDIELTQS-PAIM 142  
 Db 140 GSASAPTLPLVSCNSPSSDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVL 199  
 QY 143 SASPGERVMTCSASSV-----  
 Db 200 RGGKYAATSQVLLPSKDVMOGTDEHWCKVQHPNGNKEKVPFLVIAELPKVSVFVPPR 259  
 QY 161 -----RYMNFQOKSGTSPKR-----WIYDTSKLSGVPAFPFGSGSGTYSLTISME 209  
 Db 260 DGFFGNPKSKLIQATGFSPRQIQVSWLREGKQVGGV-----TTQVQ 304  
 QY 210 AEDAATYCCQWSSNLTFTGAGTKLEKRAAAEQKLISEDLNGAVDEQKLISEDLNAV 269  
 Db 305 AEAK-----ESGPTTYKVTSLTIK-----ESDWSQSMTCEVDHRLGLTFQGNASSM 352  
 QY 270 ---GQDTQ-EVIVVPHSLPFKVVVISAILALVLTITSLIILIMLWOKK 314  
 Db 353 CVPDQDTAIRVFAIPPSFASIFLTKSTKLTCLVTDLTATYDSVTISWTRQ 401  
 RESULT 13  
 Q8KLF3 PRELIMINARY; PRT; 112 AA.  
 AC Q8KLF3  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Anti-VIPase light chain variable region (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;

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RN RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RT "Innate proteolytic antibodies: Failed D-Vipase response to the D-
RL entantlomer of VIP and identification of L-Vipase VL domains.";
DR EMBL; AF516282; AAM64200.1; -.
DR PIR; A33933; A33933.
DR PIR; PH1085; PH1085.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12017 MW; 22DD75B5414CDB18 CRC64;

Query Match 28.4%; Score 461; DB 11; Length 112;
Best Local Similarity 81.8%; Pred. No. 3.9e-29;
Matches 90; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 132 DIETQSPALMSASGPERVTTCASSSVRYNMVQKSGTSPKRWIYDTSKLSSGVP 191
DB 1 DIVLTQSPALMSASGPERVTTCASSSVRYNMVQKSGTSPKRWIYDTSKLSSGVP 60

QY 192 FSGSGSGTSYSLTISSEAEADAATYYCOQWSSNPLTFCAGTKLEKRAA 241
DB 61 FSGSGSGTSYSLTISSEAEADAATYYCOQWSSNPLTFCAGTKLEKRAA 110

RESULT 14
Q8K1F1 PRELIMINARY; PRT; 114 AA.
AC Q8K1F1
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 25, Last annotation update)
DE Anti-Vipase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RT "Innate proteolytic antibodies: Failed D-Vipase response to the D-
RL entantlomer of VIP and identification of L-Vipase VL domains.";
DR EMBL; AF516284; AAM64202.1; -.
DR PIR; A33933; A33933.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 12162 MW; 8BD9833DBF3BEFD1 CRC64;

Query Match 28.2%; Score 458; DB 11; Length 114;
Best Local Similarity 81.2%; Pred. No. 6.9e-29;
Matches 91; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 132 DIETQSPALMSASGPERVTTCASSSV--RYNMVQKSGTSPKRWIYDTSKLSSGVP 189
DB 1 DIVLTQSPALMSASGPERVTTCASSSVSSYLLHWYQKSGSPKRWIYDTSKLSSGVP 60

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QY 190 ARFSGSGSGTSYSLTISSEAEADAATYYCOQWSSNPLTFCAGTKLEKRAA 241
DB 61 ARFSGSGSGTSYSLTISSEAEADAATYYCOQWSSNPLTFCAGTKLEKRAA 112

RESULT 15
Q9R1A4 PRELIMINARY; PRT; 437 AA.
AC Q9R1A4
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gamma heavy chain of Mab7 (Fragment).
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -.
DR PIR; B45837; B45837.
DR PDB; 1COK; 11-SEP-99.
DR PDB; 1I91; 25-DEC-02.
DR PDB; 1KCU; 11-MAY-02.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match 28.0%; Score 454.5; DB 11; Length 437;
Best Local Similarity 44.4%; Pred. No. 7.6e-28;
Matches 108; Conservative 23; Mismatches 69; Indels 43; Gaps 7;

QY 4 VKLQESGGGLVQPGGSRKLSCAASGFTFSSFGHWVROAPEKLEWVAYISSGSIYYA 63
DB 1 VQLQESGGGLVQPGGSLKLSCAASGFTFSSYAMSWRQTPKRLWVASFSSG-GIIYIT 59
QY 64 DTVKGRFTISRDNPKNTLFLQMTSLRSBDTVMYYCAR-DYGAYWCGGTVTTVSSGGSGG 122
DB 60 DSVKGRFTIYKDKRNLISLQMSLSRSEDAMYYCARGDYSAWYGGTGLVTVSAA----- 114
QY 123 GGGSGGGSDIELTQSPALMSASGPERVTTCASSSVRYNMVQKSGTSPKRWIYDTS 182
DB 115 -----KTPFPSPVPLAPGSAAGTNSMTGLGLVKGYPFE-----PVTWNHG 157
QY 183 KLSSGV---PARFSGSGSGTSYSLTISSEAEADAATYYCOQWSSNPLTF-----GAGTKL 234
DB 158 SLSSGVHTFPVQLQSDLYTLSSSVTVPS-----STWPSBTVCNVAHPASSTKV 206
QY 235 ELK 237
DB 207 DXK 209

Search completed: May 27, 2004, 05:58:09
Job time : 52 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 27, 2004, 05:54:07 ; Search time 60 seconds  
(without alignments)  
1488.084 Million cell updates/sec

Title: US-09-403-882A-2

Perfect score: 1622

Sequence: 1 MAEVKIQESGGLVQPGSR.....VLTITSLILMLWQKKPR 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_29Jan04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1622	100.0	316	2	Aav32086 Single ch
2	1319	81.3	255	3	Aab11398 E. coli e
3	1319	81.3	255	4	Aab74199 PelB-scfv
4	1319	81.3	255	4	Aab70769 Expressio
5	1319	81.3	255	4	Aay72020 E. caroto
6	1237	76.3	241	6	Abr62010 Single-ch
7	1227	75.6	241	5	Aam48925 scfv anti
8	1194	73.1	236	2	Aar32842 VH NQ10/1
9	1195	73.1	240	2	Aar68613 Single ch
10	1097	67.7	223	2	Aar32841 VH NQ10/1
11	1008	62.1	580	2	Aaw90217 Bispecifi
12	1001	61.7	556	2	Aaw90218 Bispecifi
13	976.5	60.2	237	7	Aae38657 Mouse G1
14	970.5	59.8	268	3	Aay44973 Recombina
15	967.5	59.6	268	3	Aay44972
16	964.5	59.5	284	2	Aar95569 Intracell
17	954	58.8	280	6	Abr42055 Newcastle
18	939	57.3	234	2	AAR64819
19	938.5	57.9	235	2	AAR32840
20	937	57.8	258	2	Aaw90221
21	935.5	57.7	294	4	AAR320442
22	934.5	57.6	293	4	AAG65715
23	928.5	57.2	282	6	ABJ19276 Anti-huma
24	919	56.7	553	2	Aaw11508 Single ch
25	919	56.7	553	2	Aaw73223 H22-anti-

25	919	56.7	553	4	AB61360 Bispecifi
26	919	56.7	553	4	AB85455 Bispecifi
27	913	56.3	242	6	ABR62132 Single ch
28	907	55.9	353	2	Aay06273 Anti Fc a
29	906.5	55.9	237	5	ABP46093 Human BLY
30	906.5	55.9	253	2	Aaw90225 Anti-B7.1
31	903.5	55.7	237	5	ABP46009 Human BLY
32	903.5	55.5	237	5	ABP46103 Human BLY
33	900.5	55.5	237	5	ABP45994 Human BLY
34	900.5	55.5	281	2	Aaw82744 Fusion pr
35	899.5	55.5	237	5	ABP46107 Human BLY
36	898.5	55.4	237	5	ABP46104 Human BLY
37	897.5	55.3	237	5	ABP46106 Human BLY
38	897.5	55.3	237	5	ABP46016 Human BLY
39	897.5	55.3	245	2	Aay06717 Antibody
40	897.5	55.3	245	2	Aau72874 3B10x25-2
41	897.5	55.3	503	5	AAY17963 Mouse scf
42	897	55.3	239	2	Aau72866 F5-3 sing
43	897	55.3	256	5	ABP46017 Human BLY
44	896.5	55.3	237	5	ABP45992 Human BLY
45	896.5	55.3	237	5	ABP45992 Human BLY

## ALIGNMENTS

## RESULT 1

AAY32086

ID AAY32086 standard; protein; 316 AA.

AC AAY32086;

DT 17-JAN-2000 (first entry)

DE Single chain antibody used in probe detection.

DX Single chain antibody; scAb; sfv; spectroscopic probe.

OS Unidentified.

PN WO9951986-A1.

PD 14-OCT-1999.

PF 08-APR-1999; 99WO-US007847.

PR 08-APR-1998; 98US-0081118P.

PS 09-APR-1998; 98US-0081340P.

PA (REGC ) UNIV CALIFORNIA.

PI Farinas J;

DR WPI; 1999-611066/52.

PT N-PSDB; AAZ20266.

Localizing probes to specific sites in cells that express single-chain antibody reactive with probe-ligand conjugate, particularly for detecting post-translational modification and its modulators.

Claim 5; Page 47-48; 69pp; English.

The present sequence represents a single chain antibody (scAb) that has 2 c-myc epitopes. The scAb is used in claimed methods for localizing a probe and for detecting a post-translational activity in a cell, and is expressed by a claimed transgenic non-human animal. The invention provides methods and reagents for targeting probes to selected cellular locations through the expression of specific binding partners (such as scAbs) within a cell, and for creating assays for post-translational activities. The invention allows the monitoring of the location of such intracellular, specific binding partners over time and in response to stimuli, such as test chemicals. Spectroscopic probes can be used to screen a test chemical for activity. The invention also includes cells and transgenic organisms comprising the intracellular specific binding

CC partner, where the specific binding partner can bind with the  
 CC spectroscopic probe/ligand conjugate, scbbs can be expressed within the  
 CC cell and can be designed to bind a wide variety of spectroscopic probes,  
 CC including small molecules that have better (and more diverse)  
 CC spectroscopic properties than green fluorescent protein  
 XX  
 SQ Sequence 316 AA;

Query Match 100.0%; Score 1622; DB 2; Length 316;  
 Best Local Similarity 100.0%; Pred. No. 2e-108;  
 Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAEVKLSGGGLVQPGGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAYISSGSSSTI 60  
 Db 1 MAEVKLSGGGLVQPGGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAYISSGSSSTI 60  
 QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGAYWGQGTVTTVSSGGGG 120  
 Db 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGAYWGQGTVTTVSSGGGG 120  
 QY 121 SGGGSGGGSDIELTQSPAIMSASPGERVMTWTCASSSVRYMNVFQKSGTSPKRWIYD 180  
 Db 121 SGGGSGGGSDIELTQSPAIMSASPGERVMTWTCASSSVRYMNVFQKSGTSPKRWIYD 180  
 QY 181 TSKLSSGVPARFSGSGGTSYSLTISSEAEADAATYICQWSSNPLTFGAGTKLELKRAA 240  
 Db 181 TSKLSSGVPARFSGSGGTSYSLTISSEAEADAATYICQWSSNPLTFGAGTKLELKRAA 240  
 QY 241 AEQKLISEEDLNGAVDEQKLISEEDLNGAVGDTQEVIVWPHSLPFKVVVISAILALVLT 300  
 Db 241 AEQKLISEEDLNGAVDEQKLISEEDLNGAVGDTQEVIVWPHSLPFKVVVISAILALVLT 300  
 QY 301 IISLIILMLWQKKPR 316  
 Db 301 IISLIILMLWQKKPR 316

RESULT 2  
 AAB11398  
 ID AAB11398 standard; protein; 255 AA.  
 AC AAB11398;  
 DT 22-FEB-2001 (first entry)  
 DE E. coli expression plasmid pUBS520-ScFvOx encoded protein.  
 XX  
 KW Eukaryotic protein; protease; interferon; antibody; hormone;  
 KW disulfide bridge.  
 XX Escherichia coli.  
 OS Synthetic.  
 XX  
 PN EP1048732-A1.  
 PD 02-NOV-2000.  
 PF 26-APR-1999; 99EP-00107412.  
 PR 26-APR-1999; 99EP-00107412.  
 XX  
 PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 DR WPI; 2000-674185/66.  
 DR N-PSDB; AAC66074.  
 XX  
 PT Preparation of water-soluble eukaryotic polypeptides with disulfide  
 PT bridges e.g. rPA, comprises cultivation of prokaryotic cells in the  
 PT presence of arginine or amide compound.  
 XX  
 PS Example 6; Page 22-23; 40pp; German.  
 XX  
 CC This invention describes a novel preparation of a water-soluble,

CC naturally occurring eukaryotic polypeptide containing two or more  
 CC cysteine units bound via a disulfide bridge which comprises cultivation  
 CC of prokaryotic cells in the presence of arginine or an amide compound.  
 CC The method is useful for the preparation of eukaryotic proteins e.g.  
 CC proteases, interferons, protein hormones, antibodies or antibody  
 CC fragments (e.g. a single chain FV fragment that binds to thyroid  
 CC stimulating hormone). It is especially useful for preparing proteins with  
 CC more than five disulfide bridges, e.g. recombinant plasminogen activator  
 CC (rPA). The technique is simple and does not require in vitro after-  
 CC treatment, such as the removal of inclusion bodies, reduction or  
 XX naturalization  
 SQ Sequence 255 AA;

Query Match 81.3%; Score 1319; DB 3; Length 255;  
 Best Local Similarity 99.2%; Pred. No. 8.8e-87;  
 Matches 252; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MAEVKLSGGGLVQPGGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAYISSGSSSTI 60  
 Db 1 MAEVKLSGGGLVQPGGSRKLSCAASGFTFSFGMHVVRQAPKGLWVAYISSGSSSTI 60  
 QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGAYWGQGTVTTVSSGGGG 120  
 Db 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYICARDYGAYWGQGTVTTVSSGGGG 120  
 QY 121 SGGGSGGGSDIELTQSPAIMSASPGERVMTWTCASSSVRYMNVFQKSGTSPKRWIYD 180  
 Db 121 SGGGSGGGSDIELTQSPAIMSASPGERVMTWTCASSSVRYMNVFQKSGTSPKRWIYD 180  
 QY 181 TSKLSSGVPARFSGSGGTSYSLTISSEAEADAATYICQWSSNPLTFGAGTKLELKRAA 240  
 Db 181 TSKLSSGVPARFSGSGGTSYSLTISSEAEADAATYICQWSSNPLTFGAGTKLELKRAA 240  
 QY 241 AEQKLISEEDLNGA 254  
 Db 241 AEQKLISEEDLNGA 254

RESULT 3  
 AAB74199  
 ID AAB74199 standard; protein; 255 AA.  
 AC AAB74199;  
 DT 29-MAY-2001 (first entry)  
 DE PelB-scFvOxazolon fusion protein.  
 XX  
 KW Molecular chaperone; PelB signal sequence; scFvOxazolon.  
 XX  
 OS Unidentified.  
 XX  
 PN EP1077262-A1.  
 PD 21-FEB-2001.  
 PF 24-JUL-2000; 2000EP-00115839.  
 PR 29-JUL-1999; 99EP-00114811.  
 XX  
 PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 XX  
 PI Ambrosius D, Rudolph R, Schaeffner J, Schwarz E;  
 XX  
 DR WPI; 2001-246712/26.  
 DR N-PSDB; AAF77806.  
 XX  
 PT Producing naturally folded eukaryotic proteins e.g. antibodies,  
 PT interferon, hormones or proteases that contain two or several cysteines  
 PT linked by disulfide bridges comprises co-expression of a molecular  
 PT chaperone.  
 XX

PS Disclosure; Page 19; 35pp; English.

XX The present invention relates to a method for production of a naturally  
 CC folded eukaryotic protein containing two or more cysteines linked by  
 CC disulfide bridges. The method comprises co-expression and secretion into  
 CC the periplasm of a molecular chaperone via an expression vector coding  
 CC for the chaperone. The expression vector also encodes a signal sequence.  
 CC The method is useful for producing a naturally folded eukaryotic protein  
 CC such as an antibody, antibody fragment, interferon, protein hormone or a  
 CC protease containing two or several cysteines linked by disulfide bridges.  
 CC The present sequence is a fusion protein composed of the PelB signal  
 CC sequence and ScFvOxazolon. This sequence was used in the method of the  
 CC present invention

XX SQ Sequence 255 AA;

Query Match 81.3%; Score 1319; DB 4; Length 255;  
 Best Local Similarity 99.2%; Pred. No. 8.8e-87;  
 Matches 252; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSFGHWHVWVQAPKGLWVAYISSGSTI 60  
 DB 1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSFGHWHVWVQAPKGLWVAYISSGSTI 60

QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVMTYCYARDYCAWYWGQTTTVSSGGGG 120  
 DB 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVMTYCYARDYCAWYWGQTTTVSSGGGG 120

QY 121 SGGGGGGGGSDIELTQSPAIMSASGERVTMTCSASSSVRYMNVFQOKSGTSPKRWIYD 180  
 DB 121 SGGGGGGGGSDIELTQSPAIMSASGERVTMTCSASSSVRYMNVFQOKSGTSPKRWIYD 180

QY 181 TSKLSSGVPARFSGSGSGTYSYLTSSMEADAATYCCQWSSNPLTFTGAGTKLELRAA 240  
 DB 181 TSKLSSGVPARFSGSGSGTYSYLTSSMEADAATYCCQWSSNPLTFTGAGTKLELRAA 240

QY 241 ASQKLISEEDLNGA 254  
 DB 241 AEQKLISEEDLNGA 254

RESULT 4  
 AAB70769  
 ID AAB70769 standard; protein; 255 AA.  
 AC AAB70769;  
 XX  
 DT 18-MAY-2001 (first entry)  
 XX  
 DE Expression plasmid pUBS520-ScFvOx protein.  
 XX  
 KW Chaperone protein; periplasm; antibody production; protein production;  
 KW interferon production; protease production.  
 XX  
 OS Escherichia coli.  
 OS Synthetic.  
 XX  
 XX EP1077263-A1.  
 XX  
 XX 21-FEB-2001.  
 XX  
 XX 29-JUL-1999; 99EP-00114811.  
 XX  
 XX 29-JUL-1999; 99EP-00114811.  
 XX  
 XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 XX  
 XX WPI: 2001-204356/21.  
 XX N-PSDB; AAF61193.  
 XX  
 XX Preparation of naturally folded eukaryotic proteins, e.g. antibodies, by  
 PT simultaneous expression of a chaperone protein, allows simple recovery  
 PT from periplasm or medium.

XX PS Disclosure; Page 20-21; 36pp; German.

XX This invention describes a novel method for preparing a naturally folded  
 CC eukaryotic polypeptide (I) that contains two or more disulfide-bridged  
 CC Cys residues by culturing prokaryotic cells that contain an expression  
 CC vector for (I) including a prokaryotic signal sequence at its N-terminus  
 CC and a nucleic acid (II) that secretes a chaperone protein (III) into the  
 CC periplasm. (I) is secreted into the periplasm or medium; the signal  
 CC peptide is then cleaved and (I) isolated from the periplasm or medium.  
 CC The method is used for production of antibody, interferon, protein  
 CC hormone or protease. Expression of (III) increases the yield of (I). The  
 CC method is simple and eliminates time-consuming in vitro processing  
 CC operations such as dissolution of inclusion bodies, reduction and  
 CC refolding. (III) protects (I) against agglomeration and promotes their  
 CC natural conformation

XX SQ Sequence 255 AA;

Query Match 81.3%; Score 1319; DB 4; Length 255;  
 Best Local Similarity 99.2%; Pred. No. 8.8e-87;  
 Matches 252; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSFGHWHVWVQAPKGLWVAYISSGSTI 60  
 DB 1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSFGHWHVWVQAPKGLWVAYISSGSTI 60

QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVMTYCYARDYCAWYWGQTTTVSSGGGG 120  
 DB 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVMTYCYARDYCAWYWGQTTTVSSGGGG 120

QY 121 SGGGGGGGGSDIELTQSPAIMSASGERVTMTCSASSSVRYMNVFQOKSGTSPKRWIYD 180  
 DB 121 SGGGGGGGGSDIELTQSPAIMSASGERVTMTCSASSSVRYMNVFQOKSGTSPKRWIYD 180

QY 181 TSKLSSGVPARFSGSGSGTYSYLTSSMEADAATYCCQWSSNPLTFTGAGTKLELRAA 240  
 DB 181 TSKLSSGVPARFSGSGSGTYSYLTSSMEADAATYCCQWSSNPLTFTGAGTKLELRAA 240

QY 241 AEQKLISEEDLNGA 254  
 DB 241 AEQKLISEEDLNGA 254

RESULT 5  
 AAY72020  
 ID AAY72020 standard; protein; 255 AA.  
 AC AAY72020;  
 XX  
 DT 28-MAR-2001 (first entry)  
 XX  
 DE E. carotovora PelB-scfVox fusion protein encoded by pUBS520-pIN-scfVox.  
 XX  
 KW Secreted protein; chaperone; interferon; protease; hormone;  
 KW naturally folded protein; lac promoter; DnaJ; heat shock protein; HSP;  
 KW pectate lyase B; PelB; haptens; single-chain Fv-fragment Oxazolon;  
 KW scFvOxazolon; fusion protein; thyroid stimulating hormone; TSH.  
 XX  
 OS Pectobacterium carotovorum.  
 OS Unidentified.  
 OS Chimeric.  
 XX  
 XX EP1054063-A2.  
 XX  
 XX 22-NOV-2000.  
 XX  
 XX 19-APR-2000; 2000EP-00108505.  
 XX  
 XX 26-APR-1999; 99EP-00107412.  
 XX  
 XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.

PI Ambrosius D, Rudolph R, Schaeffner J, Schwarz E;  
 XX WPI; 2001-033777/05.  
 DR N-PSDB; AAD02212.  
 XX  
 XX Producing water-soluble, naturally folded, and secreted eukaryotic  
 PT polypeptide, involves culturing prokaryotic cells containing an  
 PT expression vector encoding the polypeptide in the presence of arginine or  
 PT a specific compound.  
 XX  
 XX Example 6; Page 22-23; 35pp; English.

XX The patent discloses a method for the production of a water-soluble,  
 CC naturally folded and secreted eukaryotic proteins in prokaryotic cells.  
 CC The method involves culturing the prokaryotic cells, containing an  
 CC expression vector encoding the desired protein and the prokaryotic signal  
 CC sequence, in the presence of an additive, e.g., L-arginine. The signal  
 CC sequence mediates the secretion of the desired protein into the  
 CC periplasm, where folding of the protein takes place. The prokaryotic cell  
 CC also contains an expression vector encoding a molecular chaperone, e.g.,  
 CC DnaJ and heat shock protein 25 (HSP25). The simultaneous co-  
 CC overexpression and co-secretion of molecular chaperones in the periplasm  
 CC improves the yield of functionally folded protein. The above method  
 CC recombinantly produces a high yield of eukaryotic secreted proteins in  
 CC prokaryotes. The method is useful for producing eukaryotic proteins such  
 CC as an antibody, antibody fragment, interferon, protein hormone or a  
 CC protease. The present sequence is an Erwinia carotovora pectate lyase B  
 CC (PelB) signal sequence-scFvOX fusion protein encoded by PUBS520-pIN-  
 CC scFvOX. The plasmid, PUBS520-pIN-scFvOX, also comprises the lac promoter.  
 CC The single-chain Fv-fragment, which is directed against the haptan  
 CC oxazolone (scFvOxazolone), is an antibody fragment against thyroid  
 CC stimulating hormone (TSH). The co-expression of scFvOX which has no  
 CC chaperone properties is used as a negative control  
 XX  
 XX Sequence 255 AA;

Query Match 81.3%; Score 1319; DB 4; Length 255;  
 Best Local Similarity 99.2%; Pred. No. 8.8e-87;  
 Matches 252; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MAEVLQESGGGLVQPGGSRKLSCAASGFTFSFGMHWVRQAPKGLWVAYISSGSSTI 60  
 Db 1 MAEVLQESGGGLVQPGGSRKLSCAASGFTFSFGMHWVRQAPKGLWVAYISSGSSTI 60  
 QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVWYVCARDYAGWQCGTTVTVSSGGGG 120  
 Db 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVWYVCARDYAGWQCGTTVTVSSGGGG 120  
 QY 121 SGGGGGGGGSDIELTQSPAIMSASPGERVMTTCSASSSVRYMNFQKSGTSPKRWIYD 180  
 Db 121 SGGGGGGGGSDIELTQSPAIMSASPGERVMTTCSASSSVRYMNFQKSGTSPKRWIYD 180  
 QY 181 TSKLSSGVPARFSGSGSGTSYSLTSSMEADAATYTCQWSSNPLTFGAGTKLELKRAA 240  
 Db 181 TSKLSSGVPARFSGSGSGTSYSLTSSMEADAATYTCQWSSNPLTFGAGTKLELKRAA 240  
 QY 241 AEQKLISEEDLNGA 254  
 Db 241 AEQKLISEEDLNGA 254

RESULT 6  
 ABR62010  
 ID ABR62010 standard; protein; 241 AA.  
 XX  
 XX ABR62010;  
 XX  
 XX 03-OCT-2003 (first entry)  
 XX  
 XX Single-chain (scFv) antibody.  
 DE  
 XX Transgenic; biomolecule; ATP; ADP; cytosstatic; virucide; gene therapy;  
 XX antisense therapy; scFv; antibody.  
 KW

XX Synthetic.  
 OS  
 XX EP1321524-A1.  
 PN  
 XX 25-JUN-2003.  
 PD  
 XX 19-DEC-2001; 2001EP-00130319.  
 XX  
 XX 19-DEC-2001; 2001EP-00130319.  
 XX  
 XX (DUEB/) DUERING K.  
 PA  
 XX Mahn A, Hantke S, Petsch D;  
 PI  
 XX WPI; 2003-543829/52.  
 DR  
 XX N-PSDB; ACC84876.  
 XX

Increasing the content of transgene-coded biomolecules in a plant or  
 PT animal, useful for producing proteins for diagnosing, preventing and/or  
 PT treating viral diseases and cancer, comprises changing the distribution  
 PT of ATP and/or ADP.  
 PT  
 XX

Example 2; Fig 2; 18pp; English.  
 XX  
 XX The invention relates to increasing the content of one or more transgene-  
 CC coded biomolecules in an organism and involves changing the distribution  
 CC of ATP and/or ADP in cells of the organism. The yield of transgenic  
 CC molecules in host cells is often insufficient for industrial production.  
 CC The method increases the yield of transgenic molecules in animal and  
 CC plant host cells, therefore facilitating their production on an  
 CC industrial scale. The proteins produced by the method are useful for  
 CC diagnosing, preventing and/or treating viral diseases and cancer. The  
 CC present sequence represents a single-chain (scFv) antibody, used to  
 CC exemplify the increase in the expression of scFv antibodies in transgenic  
 CC potato tubers  
 XX

Sequence 241 AA;

Query Match 76.3%; Score 1237; DB 6; Length 241;  
 Best Local Similarity 97.9%; Pred. No. 6.3e-81;  
 Matches 235; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 AEVLQESGGGLVQPGGSRKLSCAASGFTFSFGMHWVRQAPKGLWVAYISSGSSTIY 61  
 Db 2 AEVLQESGGGLVQPGGSRKLSCAASGFTFSFGMHWVRQAPKGLWVAYISSGSSTIY 61  
 QY 62 YADTVKGRFTISRDNPKNTLFLQMTSLRSEDVWYVCARDYAGWQCGTTVTVSSGGGG 121  
 Db 62 YADTVKGRFTISRDNPKNTLFLQMTSLRSEDVWYVCARDYAGWQCGTTVTVSSGGGG 121  
 QY 122 GGGGGGGGGSDIELTQSPAIMSASPGERVMTTCSASSSVRYMNFQKSGTSPKRWIYD 181  
 Db 122 GGGGGGGGGSDIELTQSPAIMSASPGERVMTTCSASSSVRYMNFQKSGTSPKRWIYD 181  
 QY 182 SKLSSGVPARFSGSGSGTSYSLTSSMEADAATYTCQWSSNPLTFGAGTKLELKRAA 241  
 Db 182 SKLSSGVPARFSGSGSGTSYSLTSSMEADAATYTCQWSSNPLTFGAGTKLELKRAA 241

RESULT 7  
 AAM48925  
 ID AAM48925 standard; protein; 241 AA.  
 XX  
 XX AAM48925;  
 XX  
 XX 03-MAY-2002 (first entry)  
 XX  
 XX scFv antibody.  
 DE  
 XX Ketone binding protein; oxazole; pathogen resistance; virucide;  
 KW fungicide; antibacterial; scFv antibody.  
 XX

OS Unidentified.  
 XX Key Location/Qualifiers  
 FH Misc-difference 137 /note= "encoded by CAG"  
 FT Misc-difference 201 /note= "encoded by TAC"  
 FT  
 XX WO200204020-A2.  
 XX  
 XX 17-JAN-2002.  
 XX  
 XX 17-MAY-2001; 2001WO-DE001916.  
 XX  
 XX 12-JUL-2000; 2000DE-01033750.  
 XX  
 XX (NPBC-) MPB COLOGNE GMBH.  
 XX  
 XX Duerling K, Brinkmann O;  
 XX WPI; 2002-154868/20.  
 XX N-PSDB; AAK98639.  
 XX  
 XX Imparting pathogen resistance to plants and animals, comprises using a  
 PT polypeptide that binds to an oxazole-derived ketone, optionally expressed  
 PT from nucleic acid.  
 XX  
 XX Example 3; Fig 1; 20pp; German.  
 PS  
 XX The present invention relates to the use of a polypeptide that binds a  
 CC ketone derived from oxazole for generating pathogen resistance in an  
 CC organism. This can be used to impart resistance to pathogens (bacteria,  
 CC fungi or viruses) to a wide range of plants (e.g. cereals, sugar beet,  
 CC tobacco etc.), humans, farm animals and pets. Exemplified are activities  
 CC against Phytophthora infestans and Erwinia carotovora in potatoes and  
 CC Staphylococcus aureus in mice. The present sequence is a sc-Fv antibody,  
 CC which is capable of binding 2-phenyloxazol-5-one  
 XX  
 XX Sequence 241 AA;  
 XX  
 Query Match 75.6%; Score 1227; DB 5; Length 241;  
 Best Local Similarity 97.1%; Pred. No. 3.3e-80;  
 Matches 234; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MAEVLQESGGGLVQPGSRKLSCAASGFTFSFGHWRQAPKGLWVAYISSGSTI 60  
 DB 1 MADVLVESGGGLVQPGSRKLSCAASGFTFSFGHWRQAPKGLWVAYISSGSTI 60  
 QY 61 YYADTVKGRFTISRDNPKNTLFLQWTSLSRSEDVYMYCARYGATGQGTVTYSSGGGG 120  
 DB 61 YYADTVKGRFTISRDNPKNTLFLQWTSLSRSEDVYMYCARYGATGQGTVTYSSGGGG 120  
 QY 121 SGGGGSGGGSDIELTQSPAINMSAPGKVTMTCSASSSVRYMNFQOKSGTSPKRWIYD 180  
 DB 121 SGGGGSGGGSDIELTQSPAINMSAPGKVTMTCSASSSVRYMNFQOKSGTSPKRWIYD 180  
 QY 181 TKLSGVPARPSGGSGGTYSLTISMEADAATYTCQWSSNPLTFCAGTKLEKRAA 240  
 DB 181 TKLSGVPARPSGGSGGTYSLTISMEADAATYTCQWSSNPLTFCAGTKLEKRAA 240  
 QY 241 A 241  
 DB 241 A 241  
 RESULT 8  
 AAR32842  
 ID AAR32842 standard; protein; 236 AA.  
 XX  
 XX AAR32842;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 19-JUN-1993 (first entry)

XX VH NQ10/12.5-Vk NQ10/12.5 linked peptide sequences #2.  
 XX  
 XX Primer; human; immunoglobulin; Ig; variable region: VH; VL; Ck; JH;  
 KW lymphocyte; vector; soluble; antibody; phage; linker; back; VH3; tested;  
 KW in-cell PCR; cloning; polymorphic; TCR V; anti-phenyloxazolone; hybridoma;  
 KW NQ2/12.4; NQ10/12.5.  
 XX  
 XX Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Region 1. .115  
 FT /label= VH\_NQ10/12.5  
 FT Peptide 116. .129\_ /note= "Linker peptide"  
 FT 130. .236  
 FT Region /label= Vkappa\_NQ10/12.5  
 XX  
 XX WO9303151-A1.  
 XX 18-PBB-1993.  
 XX  
 XX 10-AUG-1992; 92WO-GB001483.  
 XX  
 XX 10-AUG-1991; 91GB-00017352.  
 XX 11-JUN-1992; 92GB-00012419.  
 XX  
 XX (MEDI-) MEDICAL RES COUNCIL.  
 XX  
 XX Embleton MJ, Gorochov G, Jones PT, Winter GP;  
 WPI; 1993-076508/09.  
 N-PSDB; AAQ37461.  
 XX  
 XX Treatment of cell populations, partic. hybridomas - to link together  
 PT copies of 2 or more non-contiguous DNA sequences to facilitate analysis.  
 XX  
 XX Disclosure; Fig 4; 72pp; English.  
 XX  
 XX The sequences given in AAR32840-43 show the mature heavy chain VH domains  
 CC and the VK light chain genes of the anti-phenyloxazolone hybridomas  
 CC NQ2/12.4 and NQ10/12.5 which have been linked via a linker peptide by in-  
 CC cell PCR. The cDNA encoding these peptides was synthesised using forward  
 CC primers annealing to the Ck gene and the JH segment, followed by assembly  
 CC with linker primers, VH back primers based on the VH3 leader sequence and  
 CC a forward Ck primer, nested in the cells is then amplified with nested primers  
 CC assembled product within the cells is then amplified with nested primers  
 CC annealing to the 5' end of the VH gene and the 3' end of the Jk segment.  
 CC In-cell PCR may be used to determine gene linkage analysis, particularly  
 CC for the cloning of gene combinations that are polymorphic within a  
 CC population of cells, such as the rearranged genes for Ig or TCR V  
 CC regions. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 236 AA;  
 XX  
 Query Match 73.6%; Score 1194; DB 2; Length 236;  
 Best Local Similarity 96.2%; Pred. No. 7.5e-78;  
 Matches 226; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
 QY 3 EVKLQESGGGLVQPGSRKLSCAASGFTFSFGHWRQAPKGLWVAYISSGSTIY 62  
 DB 1 DVQLVESGGGLVQPGSRKLSCAASGFTFSFGHWRQAPKGLWVAYISSGSTIY 60  
 QY 63 ADTVKGRFTISRDNPKNTLFLQWTSLSRSEDVYMYCARYGATGQGTVTYSSGGGGSG 122  
 DB 61 ADTVKGRFTISRDNPKNTLFLQWTSLSRSEDVYMYCARYGATGQGTVTYSSGGGGSG 120  
 QY 123 GGGSGGGSDIELTQSPAINMSAPGKVTMTCSASSSVRYMNFQOKSGTSPKRWIYDTS 182  
 DB 121 GGGSGGGSGQIVLTQSPAINMSAPGKVTMTCSASSSVRYMNFQOKSGTSPKRWIYDTS 180  
 QY 183 KLSGVPARPSGGSGGTYSLTISMEADAATYTCQWSSNPLTFCAGTKLEK 237





Query Match 67.7%; Score 1097.5; DB 2; Length 223;  
 Best Local Similarity 90.2%; Pred. No. 5.9e-71;  
 Matches 212; Conservative 4; Mismatches 6; Indels 13; Gaps 1;

QY 3 EVKLQESGGGLVQPGGSRKLSCAASGTFSSFGHVRQAPKGLWVAYISGSGSTIYY 62  
 DB 1 DVQLVESGGGLVQPGGSRKLSCAASGTFSSFGHVRQAPKGLWVAYISGSGSTIYY 60

QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVYVYCARDYGVAGVGGTIVVSSGGSGG 122  
 DB 61 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVYVYCARDYGVAGVGGTIVVSSGGSGG 114

QY 123 GGGSGGGSDIELTQSPAIMSAPGFRVTMTCSASSSVRYMNFQOKSGTSPKRWLYDTS 182  
 DB 115 -----ASQIVLTQSPAIMSAPGFRVTMTCSASSSVRYMNFQOKSGTSPKRWLYDTS 167

QY 183 KLSGGVPARTSGSGSTYSGLTSSMEADAATYTCQWSSNPLTFGAGTKLELK 237  
 DB 168 KLSGGVPARTSGSGSTYSGLTSSMEADAATYTCQWSSNPLTFGAGTKLELK 222

RESULT 11  
 AAW90217  
 ID AAW90217 standard; protein; 580 AA.  
 AC AAW90217;  
 XX  
 DT 10-MAY-1999 (first entry)  
 XX  
 DE Bispecific tetraivalent antibody BitAB7-24-IG10H6.  
 XX  
 KW B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;  
 KW T cell activation; inhibitor; graft versus host disease;  
 KW transplant rejection; allograft rejection; autoimmune disease; allergy;  
 KW therapy; human; bispecific tetraivalent antibody; BitAB;  
 KW BitAB7-24-IG10H6.  
 XX  
 OS Mus sp.  
 OS Homo sapiens.  
 OS Synthetic.  
 OS Chimeric.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..24  
 FT /note= "peB signal peptide"  
 FT Region 25..138  
 FT /note= "VH region anti B7.1 Mab"  
 FT Peptide 139..153  
 FT /note= "(G4S3) flexible linker"  
 FT Region 154..262  
 FT /note= "VL region anti B7.1 Mab"  
 FT Misc-difference 261  
 FT /note= "encoded by CTG"  
 FT Region 263..273  
 FT /note= "human IgG3 hinge region"  
 FT Domain 274..308  
 FT /note= "helix-turn-helix dimerisation domain"  
 FT Domain 309..319  
 FT /note= "human IgG3 hinge domain"  
 FT Region 320..446  
 FT /note= "VH region anti B7.2 Mab"  
 FT Misc-difference 322..327  
 FT /note= "codons for these amino acids are not present in the DNA sequence for BitAB7-24-IG1-H6 provided in the specification"  
 FT Peptide 447..461  
 FT /note= "(G4S3)flexible linker"  
 FT Region 462..574  
 FT /note= "VL region anti B7.2 Mab"  
 FT Peptide 575..580  
 FT /note= "His6 tag"  
 XX

PN WO9858965-A2.  
 XX 30-DEC-1998.  
 PF 22-JUN-1998; 98WO-EP003791.  
 PR 20-JUN-1997; 97EP-00870092.  
 XX (INNO-) INNOGENETICS NV.  
 PA Lorre K, Sablon E, Buyse M, Bosman A;  
 PI WPI: 1999-105615/09.  
 DR N-PSDB; AAX01651.  
 XX  
 PT New molecules which bind B7.1 and B7.2 - useful to prevent and treat  
 PT immune diseases including allograft rejection.  
 XX  
 PS Example 7.1; Fig 16; 182pp; English.  
 CC This polypeptide comprises the bispecific tetraivalent antibody BitAB7-24  
 CC -IG10H6. the molecule consists of 4 scFvs, i.e. 2 anti B7.1 scFvs and 2  
 CC anti B7.2 scFvs (tetravalency). One single BitAB is a homodimer of 2  
 CC identical molecules, each containing both an anti B7.1 and anti B7.2 scFv  
 CC (bispecificity). An anti-B7.1 and anti-B7.2 scFv are linked using a  
 CC dimerisation domain (see AAW90219), which drives the homodimerisation of  
 CC the molecule. DNA (see AAX01651) encoding the BitAB has been constructed  
 CC to allow expression of the BitAB in transformed E. coli cells. The BitAB  
 CC cross-links, and/or cross-reacts, with the costimulatory molecules B7.1  
 CC and B7.2 that are expressed on the membrane of professional antigen-  
 CC presenting cells, leading to the inhibition of antigen-specific T cell  
 CC activation. The invention relates to such B7-binding molecules, methods  
 CC for their production, and their use for treating or preventing diseases  
 CC of the immune system, in particular graft rejection, graft versus host  
 CC disease, allergy and autoimmune diseases (claimed)  
 XX  
 SQ Sequence 580 AA;

Query Match 62.1%; Score 1008; DB 2; Length 580;  
 Best Local Similarity 80.2%; Pred. No. 4.8e-64;  
 Matches 194; Conservative 19; Mismatches 25; Indels 4; Gaps 2;

QY 1 MAEYKLBESGGGLVQPGGSRKLSCAASGTFSSFGHVRQAPKGLWVAYISGSGSTI 60  
 DB 21 MAQVQLQESGGGLVQPGGSRRLSCAASGTFSSFGHVRQAPKGLWVAFISVSTLI 80

QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVYVYCARD--YGAYVGGTIVVSSGG 118  
 DB 81 YYADSVKGRFTISRDNPKNTLFLQMTSLRSEDVYVYCARDGWYFDYVGGTIVVSSGG 140

QY 119 GSGSGGGGGGGSDIELTQSPAIMSAPGFRVTMTCSASSSVRYM--WFOQKSGTSPKR 176  
 DB 141 GSGSGGGGGGGSDIELTQSPSSVAASVGRVITTCVSSSRSSNLHWYQOKSETSPK 200

QY 177 WIYDTSKLSGVPARFSGSGSTYSGLTSSMEADAATYTCQWSSNPLTFGAGTKLEL 236  
 DB 201 WIYDTSNLAGVPRFSGSGSTYDITLTSSMQPDAATYTCQWSSYPLTFGAGTKLEI 260

QY 237 KR 238  
 DB 261 KR 262

RESULT 12  
 AAW90218  
 ID AAW90218 standard; protein; 556 AA.  
 XX  
 AC AAW90218;  
 XX  
 DT 10-MAY-1999 (first entry)  
 XX  
 DE Bispecific tetraivalent antibody BitAB1G10-B7-24H6.  
 XX







GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 27, 2004, 05:56:57 ; Search time 750 Seconds

(without alignments)  
117.657 Million cell updates/sec

Title: US-09-403-882A-2

Perfect score: 1622

Sequence: 1 MAEVLQESGGGLVQPGGR.....VLTITSLILMLWQKKR 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1151071 seqs, 279249464 residues

Total number of hits satisfying chosen parameters: 1151071

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	959	59.1	291	12	US-10-406-830-10
2	943.5	58.2	288	9	US-09-818-247-22
3	927	57.2	291	12	US-10-406-830-9
4	926	57.1	287	12	US-10-406-830-5
5	913	56.3	242	14	US-10-259-087A-20
6	906.5	55.9	237	10	US-09-880-748-2104
7	906.5	55.9	237	12	US-10-293-418-2104
8	903.5	55.7	237	10	US-09-880-748-2020
9	903.5	55.7	237	12	US-10-293-418-2020
10	900.5	55.5	237	10	US-09-880-748-2005
11	900.5	55.5	237	10	US-09-880-748-2114
12	900.5	55.5	237	12	US-10-293-418-2005
13	900.5	55.5	237	12	US-10-293-418-2114
14	899.5	55.5	237	10	US-09-880-748-2118
15	899.5	55.5	237	12	US-10-293-418-2118

16	898.5	55.4	237	10	US-09-880-748-2115
17	898.5	55.4	237	12	US-10-293-418-2115
18	897.5	55.3	237	10	US-09-880-748-2027
19	897.5	55.3	237	10	US-09-880-748-2111
20	897.5	55.3	237	12	US-10-293-418-2027
21	897.5	55.3	237	12	US-10-293-418-2111
22	897.5	55.3	503	12	US-10-239-456-77
23	897	55.3	256	12	US-10-239-456-61
24	896.5	55.3	237	10	US-09-880-748-2003
25	896.5	55.3	237	10	US-09-880-748-2017
26	896.5	55.3	237	10	US-09-880-748-2019
27	896.5	55.3	237	10	US-09-880-748-2028
28	896.5	55.3	237	10	US-09-880-748-2110
29	896.5	55.3	237	12	US-10-293-418-2003
30	896.5	55.3	237	12	US-10-233-418-2017
31	896.5	55.3	237	12	US-10-293-418-2019
32	896.5	55.3	237	12	US-10-293-418-2028
33	896.5	55.3	237	12	US-10-293-418-2110
34	895.5	55.2	237	10	US-09-880-748-1906
35	895.5	55.2	237	12	US-10-293-418-1906
36	894.5	55.1	237	10	US-09-880-748-2040
37	894.5	55.1	237	12	US-10-293-418-2040
38	894	55.1	240	9	US-09-192-854-2
39	894	55.1	240	9	US-09-968-561A-2
40	894	55.1	240	10	US-09-968-744A-2
41	894	55.1	240	12	US-09-968-561A-2
42	894	55.1	248	10	US-09-880-748-1421
43	894	55.1	248	12	US-10-293-418-1421
44	889.5	54.8	237	10	US-09-880-748-2043
45	889.5	54.8	237	12	US-10-293-418-2043

## ALIGNMENTS

### RESULT 1

US-10-406-830-10  
; Sequence 10, Application US/10406830  
; Publication No. US20040071696A1  
; GENERAL INFORMATION:  
; APPLICANT: ADAMS, GREGORY P.  
; APPLICANT: HORAK, EVA M.  
; APPLICANT: WEINER, LOUIS M.  
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN FV ANTIBODY MOLECULES AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 407T-000410US  
; CURRENT APPLICATION NUMBER: US/10/406.830  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US 60/370,276  
; PRIOR FILING DATE: 2002-04-05  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10  
; LENGTH: 291  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic antibody.  
US-10-406-830-10

Query Match 59.1%; Score 959; DB 12; Length 291;  
Best Local Similarity 70.1%; Pred. No. 1.8e-60;  
Matches 185; Conservative 31; Mismatches 38; Indels 10; Gaps 2;

QY 1 MAEVLQESGGGLVQPGGRKLSCAASGFTFSSFGMEHWVRQAPKGLWYVAYISGSGSTI 60

Db 21 MAQVLQESGGGMVQPGRLSLSCAASGFTFSSYAMSNVRQAPKGLWYSAISGSGST 80

QY 61 YADTVKGRFTISRDNPKNLTFLQWTSLSRSDTVMYICARD-----YGAIVGGQGT 111

Db 81 YYADSVKGRFTISRDNSKNTLYLQWLSLRADLTALYTCAREGYSNNWNWYFDLWGRGTL 140



Query Match 57.1%; Score 926; DB 12; Length 287;  
 Best Local Similarity 69.6%; Pred. No. 4e-58;  
 Matches 181; Conservative 32; Mismatches 41; Indels 6; Gaps 3;

QY 1 MAEYKQESGGLVQPGGSRKLSCAASGFTFSFGMHVWVQAPEKGLEWVAYISSGSSTI 60  
 DB 21 MAQVQLVESGGGVQPGSRSLRLSCAASGFTFSFYIHVVRQAPGKGLEWMAVTSYDGNKK 80

QY 61 YYADTVKGRFTISRDNPNTLFQMTSLRSEDVWYICARD-YG-...-AYWGQTTVTS 115  
 DB 81 YYAASVXDRFTISRDNSKNTVSLQMSLRADETAVYICARDLYGDVADLYWGQTTVTS 140

QY 116 SGGGSGGG 174  
 DB 141 SGGGSGGG 200

QY 175 KRWIYDTSKLSSGVPAFSGSGGTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKL 234  
 DB 201 KLLIYKASTLESVPSRFTSGSGGTFTLTISGLQPEDFATYCCQLSSYPLTFGGGTRV 260

QY 235 ELKAAAEQKLISEEDLNGA 254  
 DB 261 EIKAAAEQKLISEEDLNGA 280

RESULT 5  
 US-10-259-087A-20  
 ; Sequence 20, Application US/10259087A  
 ; Publication No. US20030130190A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Vanderbilt University  
 ; APPLICANT: Hallahan, Dennis E  
 ; APPLICANT: Qu, Shiman  
 ; TITLE OF INVENTION: IN VIVO PANNING FOR LIGANDS TO RADIATION-INDUCED MOLECULES  
 ; CURRENT APPLICATION NUMBER: US/10/259,087A  
 ; CURRENT FILING DATE: 2002-09-27  
 ; PRIOR APPLICATION NUMBER: US 60/328123  
 ; PRIOR FILING DATE: 2001-10-03  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 20  
 ; LENGTH: 242  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Artificial antibody ligand number 2  
 US-10-259-087A-20

Query Match 56.3%; Score 913; DB 14; Length 242;  
 Best Local Similarity 71.1%; Pred. No. 2.8e-57;  
 Matches 172; Conservative 30; Mismatches 36; Indels 4; Gaps 2;

QY 1 MAEYKQESGGLVQPGGSRKLSCAASGFTFSFGMHVWVQAPEKGLEWVAYISSGSSTI 60  
 DB 1 MAQVQLQSGPELVKPGASVKYSCKASGYFTSYVMEHWKPKGQGLEWIGYINPYDGT 60

QY 61 YYADTVKGRFTISRDNPNTLFQMTSLRSEDVWYICARD--DYGA--YWGQTTVTS 116  
 DB 61 KYNEKFKGKAALTSDKSSSTAYMELSLTSDSAVYICARFGNYGALDYWGQTTVTS 120

QY 117 GGGGSGGG 176  
 DB 121 GGGGSGGG 180

QY 177 WIYDTSKLSSGVPAFSGSGGTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLEK 236  
 DB 181 WIYGTSLASGVPRFSGSGGTSYSLTISSEAEADAATYCCQWSSYPLTFGGGTLKLEI 240

QY 237 KR 238  
 DB 241 KR 242

RESULT 6  
 US-09-880-748-2104  
 ; Sequence 2104, Application US/09880748  
 ; Publication No. US20030059937A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruben et al.  
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
 ; FILE REFERENCE: PF523  
 ; CURRENT APPLICATION NUMBER: US/09/880,748  
 ; CURRENT FILING DATE: 2001-06-15  
 ; PRIOR APPLICATION NUMBER: 60/212,210  
 ; PRIOR FILING DATE: 2000-06-15  
 ; PRIOR APPLICATION NUMBER: 60/240,816  
 ; PRIOR FILING DATE: 2000-10-17  
 ; PRIOR APPLICATION NUMBER: 60/276,248  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: 60/277,379  
 ; PRIOR FILING DATE: 2001-03-21  
 ; PRIOR APPLICATION NUMBER: 60/293,499  
 ; PRIOR FILING DATE: 2001-05-25  
 ; NUMBER OF SEQ ID NOS: 3239  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2104  
 ; LENGTH: 237  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-880-748-2104

Query Match 55.9%; Score 906.5; DB 10; Length 237;  
 Best Local Similarity 72.6%; Pred. No. 7.8e-57;  
 Matches 172; Conservative 28; Mismatches 36; Indels 1; Gaps 1;

QY 3 EYKQESGGLVQPGGSRKLSCAASGFTFSFGMHVWVQAPEKGLEWVAYISSGSSTIY 62  
 DB 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSYVEMHWVQAPEKGLEWYISSGSSTIY 60

QY 63 ADTVKGRFTISRDNPNTLFQMTSLRSEDVWYICARDYGNVCOGTTVTVSSGGGGSG 122  
 DB 61 ADSVKGRTISRDNAKNSLYLQMSLRADETAVYICARDTDDYWGQTTVTVSSGGGGSG 120

QY 123 GGGSGGG 181  
 DB 121 GGGSGGG 180

QY 182 SKLSSGVPAFSGSGGTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLEIKR 238  
 DB 181 STLESQVPSRFTSGSGGTFTLTISLQPEDFATYCCQSYSTPWTFGGTLKLEIKR 237

RESULT 7  
 US-10-293-418-2104  
 ; Sequence 2104, Application US/10293418  
 ; Publication No. US20030223996A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruben et al.  
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
 ; FILE REFERENCE: PF523P2  
 ; CURRENT APPLICATION NUMBER: US/10/293,418  
 ; CURRENT FILING DATE: 2002-11-27  
 ; PRIOR APPLICATION NUMBER: 60/331,469  
 ; PRIOR FILING DATE: 2001-11-16  
 ; PRIOR APPLICATION NUMBER: 60/340,817  
 ; PRIOR FILING DATE: 2001-12-19  
 ; PRIOR APPLICATION NUMBER: 09/880,748  
 ; PRIOR FILING DATE: 2001-06-15  
 ; PRIOR APPLICATION NUMBER: 60/293,499  
 ; PRIOR FILING DATE: 2001-05-25  
 ; PRIOR APPLICATION NUMBER: 60/277,379  
 ; PRIOR FILING DATE: 2001-03-21  
 ; PRIOR APPLICATION NUMBER: 60/276,248  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: 60/240,816

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; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2104
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2104

Query Match      55.9%; Score 906.5; DB 12; Length 237;
Best Local Similarity 72.6%; Pred. No. 1.3e-57;
Matches 172; Conservative 28; Mismatches 36; Indels 1; Gaps 1;

QY 3 EVKLQESGGGLVQPGSRKLSCAASGFTFSFGMHVROAPEKGLEWVAYISSGSTIYY 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSEYEMNVRQAPGKGLEWYSISSGSTIYY 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTVMYICARDYGAYWCGGTTVTSSGGGSG 122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 ADSVKGRFTISRDNNAKNSLYLQNSLRABDTAVYICARDTDDYWGQGTTLTVSSGGGSG 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 GGGSGGGGSDIELTQSPALMSASPGERVMTCSASSV-RYMNWFOQKSGTSPKRWIYDT 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 GGGSGGGGSDIVMTQSPSTLSASVGRVITTCRASQGISSLAWYQOKPGRAPKVLIIYA 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 182 SKLSSGVPARFSGSGSTSYSLTSSMEAEADATYYCQWSSNPLTFGAGTKLEIKR 238
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 STLSEGVPRFSGSGGDTFTLTSSLPQEDPATYYCQOSYSTPTWTFGGQTKLEIKR 237

RESULT 8
US-09-880-748-2020
; Sequence 2020, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2020
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2020

Query Match      55.7%; Score 903.5; DB 12; Length 237;
Best Local Similarity 72.6%; Pred. No. 1.3e-56;
Matches 172; Conservative 27; Mismatches 37; Indels 1; Gaps 1;

QY 3 EVKLQESGGGLVQPGSRKLSCAASGFTFSFGMHVROAPEKGLEWVAYISSGSTIYY 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSEYEMNVRQAPGKGLEWYSISSGSTIYY 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTVMYICARDYGAYWCGGTTVTSSGGGSG 122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 ADSVKGRFTISRDNNAKNSLYLQNSLRABDTAVYICARDTDDYWGQGTTLTVSSGGGSG 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 GGGSGGGGSDIELTQSPALMSASPGERVMTCSASSV-RYMNWFOQKSGTSPKRWIYDT 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 GGGSGGGGSDIVMTQSPSTLSASVGRVITTCRASQGISSLAWYQOKPGRAPKVLIIYA 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 182 SKLSSGVPARFSGSGSTSYSLTSSMEAEADATYYCQWSSNPLTFGAGTKLEIKR 238
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 STLSEGVPRFSGSGGDTFTLTSSLPQEDPATYYCQOSYSTPTWTFGGQTKLEIKR 237

RESULT 10
US-09-880-748-2005
; Sequence 2005, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2020
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2020

Query Match      55.7%; Score 903.5; DB 10; Length 237;
Best Local Similarity 72.6%; Pred. No. 1.3e-56;
Matches 172; Conservative 27; Mismatches 37; Indels 1; Gaps 1;

QY 3 EVKLQESGGGLVQPGSRKLSCAASGFTFSFGMHVROAPEKGLEWVAYISSGSTIYY 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSEYEMNVRQAPGKGLEWYSISSGSTIYY 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTVMYICARDYGAYWCGGTTVTSSGGGSG 122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 ADSVKGRFTISRDNNAKNSLYLQNSLRABDTAVYICARDTDDYWGQGTTLTVSSGGGSG 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 GGGSGGGGSDIELTQSPALMSASPGERVMTCSASSV-RYMNWFOQKSGTSPKRWIYDT 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 GGGSGGGGSDIVMTQSPSTLSASVGRVITTCRASQGISSLAWYQOKPGRAPKVLIIYA 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 182 SKLSSGVPARFSGSGSTSYSLTSSMEAEADATYYCQWSSNPLTFGAGTKLEIKR 238
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 STLSEGVPRFSGSGGDTFTLTSSLPQEDPATYYCQOSYSTPTWTFGGQTKLEIKR 237
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; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2005
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2005

Query Match      55.5%; Score 900.5; DB 10; Length 237;
Best Local Similarity 72.2%; Pred. No. 2.1e-56;
Matches 171; Conservative 28; Mismatches 37; Indels 1; Gaps 1;

QY 3 EVKLOESGGGLVQPGGSRKLSCAASGFTFSFGMHVYRQAPKGLWVAYISSGSTIYY 62
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSYENWVRQAPGKLEWVSISSGSTIYY 60

QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYCYCARDYGAYWGQGTITVTVSSGGSGG 122
Db 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYICARDTDDYWGQGTITVTVSSGGSGG 120

QY 123 GGGSGGGSDIELTOSPAIMASGERVTMTCSASSV-RYMNWFOQKSGTSPKRWIYDT 181
Db 121 GGGSGGGSDIVMTQSPSTLSASVGDRTITCRASQGISLWLAAYQKPGKAPKVLIIYKA 180

QY 182 SKLSSGVPARFSGSGSGTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLEIKR 238
Db 181 STLESQVPSRFSGSGSGTDFLTITSLQPEDFATYYCQSYSTPWTFGQTKLEIKR 237

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2005
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2005

Query Match      55.5%; Score 900.5; DB 12; Length 237;
Best Local Similarity 72.2%; Pred. No. 2.1e-56;
Matches 171; Conservative 28; Mismatches 37; Indels 1; Gaps 1;

QY 3 EVKLOESGGGLVQPGGSRKLSCAASGFTFSFGMHVYRQAPKGLWVAYISSGSTIYY 62
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSYENWVRQAPKGLWVSISSGSTIYY 60

QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYCYCARDYGAYWGQGTITVTVSSGGSGG 122
Db 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYICARDTDDYWGQGTITVTVSSGGSGG 120

QY 123 GGGSGGGSDIELTOSPAIMASGERVTMTCSASSV-RYMNWFOQKSGTSPKRWIYDT 181
Db 121 GGGSGGGSDIVMTQSPSTLSASVGDRTITCRASQGISLWLAAYQKPGKAPKVLIIYKA 180

QY 182 SKLSSGVPARFSGSGSGTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLEIKR 238
Db 181 STLESQVPSRFSGSGSGTDFLTITSLQPEDFATYYCQSYSTPWTFGQTKLEIKR 237

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2005
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2005

Query Match      55.5%; Score 900.5; DB 10; Length 237;
Best Local Similarity 72.2%; Pred. No. 2.1e-56;
Matches 171; Conservative 28; Mismatches 37; Indels 1; Gaps 1;

QY 3 EVKLOESGGGLVQPGGSRKLSCAASGFTFSFGMHVYRQAPKGLWVAYISSGSTIYY 62
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSYENWVRQAPGKLEWVSISSGSTIYY 60

QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYCYCARDYGAYWGQGTITVTVSSGGSGG 122
Db 61 ADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYICARDTDDYWGQGTITVTVSSGGSGG 120

QY 123 GGGSGGGSDIELTOSPAIMASGERVTMTCSASSV-RYMNWFOQKSGTSPKRWIYDT 181
Db 121 GGGSGGGSDIVMTQSPSTLSASVGDRTITCRASQGISLWLAAYQKPGKAPKVLIIYKA 180

QY 182 SKLSSGVPARFSGSGSGTSYSLTISSEAEADAATYCCQWSSNPLTFGAGTKLEIKR 238
Db 181 STLESQVPSRFSGSGSGTDFLTITSLQPEDFATYYCQSYSTPWTFGQTKLEIKR 237

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2114
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2114

Query Match      55.5%; Score 900.5; DB 10; Length 237;
Best Local Similarity 72.2%; Pred. No. 2.1e-56;
Matches 171; Conservative 28; Mismatches 37; Indels 1; Gaps 1;

QY 3 EVKLOESGGGLVQPGGSRKLSCAASGFTFSFGMHVYRQAPKGLWVAYISSGSTIYY 62
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSYENWVRQAPGKLEWVSISSGSTIYY 60

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
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; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2114
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2114

Query Match      55.5%; Score 900.5; DB 10; Length 237;
Best Local Similarity 72.2%; Pred. No. 2.1e-56;
Matches 171; Conservative 28; Mismatches 37; Indels 1; Gaps 1;

QY 3 EVKLOESGGGLVQPGGSRKLSCAASGFTFSFGMHVYRQAPKGLWVAYISSGSTIYY 62
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSYENWVRQAPGKLEWVSISSGSTIYY 60
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Oy 182 SKLSSGVPARFSGSGTSLTSSMEABDAATYCCQWSSNPLTFGAGTKLELKR 238  
Db 181 STLESGVPSRPSGSGTDFTLTISSLOPEDFATYCCQSYSTFWTFGGTKLEIKR 237

Search completed: May 27, 2004, 06:16:21  
Job time : 758 secs